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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:38:19 ; Search time 107.547 Seconds
(without alignments)
590.532 Million cell updates/sec

Title: US-10-074-694-5
Perfect score: 803
Sequence: 1 MANLERTFIAIKPDGVQRGL.....WFKPELVYDKSCAHDWYVE 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	803	100.0	152	3	US-09-791-118A-3
2	803	100.0	152	4	US-10-232-188-5
3	803	100.0	152	4	US-10-133-628-12
4	803	100.0	152	4	US-10-440-464-90
5	803	100.0	152	5	US-10-732-923-13345
6	798	99.4	151	5	US-10-732-923-13346
7	798	99.4	151	6	US-11-013-684-1
8	798	99.4	152	4	US-10-133-628-4
9	794	98.9	152	5	US-10-732-923-13127
10	794	98.9	190	4	US-10-363-829-352
11	793	98.8	152	3	US-09-791-118A-4
12	793	98.8	152	4	US-10-116-275-332
13	793	98.8	152	5	US-10-732-923-13113
14	791	98.5	152	4	US-10-133-628-5
15	787	98.0	152	5	US-10-732-923-13128
16	778	96.9	152	5	US-10-732-923-13117
17	762	94.9	152	5	US-10-732-923-13119
18	754	93.9	152	5	US-10-732-923-13350
19	751	93.5	153	5	US-10-732-923-13336
20	749	93.3	155	4	US-10-029-386-31961
21	744	92.3	153	5	US-10-732-923-13334
22	733	91.3	152	5	US-10-732-923-13353
23	732	91.2	152	5	US-10-732-923-13126
24	732	91.2	152	5	US-10-732-923-13355
25	729	90.8	152	3	US-09-791-118A-2
26	729	90.8	152	5	US-10-732-923-13111
27	729	90.8	166	5	US-10-732-923-13110

28	728	90.7	151	5	US-10-732-923-13354	Sequence 13354, A
29	720	89.7	152	3	US-09-791-118A-1	Sequence 1, Appli
30	720	89.7	152	4	US-10-232-188-4	Sequence 4, Appli
31	720	89.7	152	4	US-10-133-628-11	Sequence 11, Appli
32	720	89.7	152	5	US-10-370-715B-110	Sequence 110, App
33	720	89.7	152	5	US-10-732-923-13341	Sequence 13341, A
34	720	89.7	176	5	US-10-732-923-13112	Sequence 13112, A
35	720	89.7	177	4	US-10-488-798-19	Sequence 19, Appli
36	720	89.7	177	4	US-10-362-892-19	Sequence 19, Appli
37	720	89.7	177	5	US-10-732-923-13342	Sequence 13342, A
38	720	89.7	178	3	US-09-833-790-426	Sequence 426, App
39	720	89.7	180	5	US-10-732-923-13340	Sequence 13340, A
40	720	89.7	180	6	US-11-013-684-2	Sequence 2, Appli
41	720	89.7	180	6	US-11-037-713-42	Sequence 42, Appli
42	717	89.3	153	5	US-10-732-923-13320	Sequence 13320, A
43	716	89.2	152	4	US-10-133-628-21	Sequence 21, Appli
44	715	89.0	152	4	US-10-133-628-2	Sequence 2, Appli
45	713.5	88.9	153	5	US-10-732-923-13132	Sequence 13132, A

ALIGNMENTS

RESULT 1
US-09-791-118A-3
; Sequence 3, Application US/09791118A
; Patent No. US20020034741A1
; GENERAL INFORMATION:
; APPLICANT: Wernier, Sabine
; APPLICANT: Braun, Susanne
; APPLICANT: Penzberg, Jörn-Peter
; APPLICANT: Goppelt, Andreas
; APPLICANT: Regenbogen, Johannes
; TITLE OF INVENTION: Use of polypeptides or nucleic acids
; TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or
; TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for
; TITLE OF INVENTION: the identification of pharmacologically
; TITLE OF INVENTION: active substances
; FILE REFERENCE: 50125/012002
; CURRENT APPLICATION NUMBER: US/09/791,118A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/199,312
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: DE 100 08 330.7
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-118A-3

Query Match	100.0%	Score 803;	DB 3;	Length 152;
Best Local Similarity	100.0%	Pred. No. 1.5e-82;		
Matches 152;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MANLERTFIAIKPDGVQRGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF	60	
Db	1	MANLERTFIAIKPDGVQRGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF	60	
Qy	61	PPGLVKYMSGPVVAMVWEGNLVGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS	120	
Db	61	PPGLVKYMSGPVVAMVWEGNLVGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS	120	
Qy	121	DSVKSAREKISLWFKPELVYDKSCAHDWYVE	152	
Db	121	DSVKSAREKISLWFKPELVYDKSCAHDWYVE	152	

RESULT 2
US-10-232-188-5
; Sequence 5, Application US/10232188

; Publication No. US20030022306A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Icyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,188
; FILING DATE: 28-Aug-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; CLONE: 127983
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-232-188-5

Query Match 100.0%; Score 803; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYIE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYIE 152

RESULT 3
US-10-133-628-12
; Sequence 12, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
; APPLICANT: GALLOIS-MONTBRUN, SARAH
; APPLICANT: SCHNEIDER, BENOIT
; APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
; APPLICANT: DEVILLE-BONNE, DOMINIQUE
; APPLICANT: VERON, MICHEL
; TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG
; TITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: 03495.0227-00000
; CURRENT APPLICATION NUMBER: US/10/133,628
; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-133-628-12

Query Match 100.0%; Score 803; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYIE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYIE 152

RESULT 4
US-10-440-464-90
; Sequence 90, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-90

Query Match 100.0%; Score 803; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYIE 152

Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
|||||
RESULT 5
US-10-732-923-13345
; Sequence 13345, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13345
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-13345
Query Match 100.0%; Score 803; DB 5; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 120
Db 61 FPLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
RESULT 6
US-10-732-923-13346
; Sequence 13346, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13346
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-13346
Query Match 99.4%; Score 798; DB 5; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.3e-82;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 61
Db 1 ANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 62 PGLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 121
Db 61 PGLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 120
Qy 122 SVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 122 SVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152

Db 121 SVKSAEKEISLWFKPEELVDYKSCAHDWYVE 151
RESULT 7
US-11-013-684-1
; Sequence 1, Application US/11013684
; Publication No. US20050136489A1
; GENERAL INFORMATION:
; APPLICANT: Industrial Technology Research Institute
; TITLE OF INVENTION: Biomarkers for Liver Diseases and Method for Using The Same
; FILE REFERENCE: 04P0019
; CURRENT APPLICATION NUMBER: US/11/013,684
; CURRENT FILING DATE: 2004-12-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human
US-11-013-684-1
Query Match 99.4%; Score 798; DB 6; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.3e-82;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 61
Db 1 ANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 62 PGLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 121
Db 61 PGLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 120
Qy 122 SVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 SVKSAEKEISLWFKPEELVDYKSCAHDWYVE 151
RESULT 8
US-10-133-628-4
; Sequence 4, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
; APPLICANT: GALLOIS-MONTBRUN, SARAH
; APPLICANT: SCHNEIDER, BENOIT
; APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
; APPLICANT: DEVILLE-BONNE, DOMINIQUE
; APPLICANT: VERON, MICHEL
; TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG
; TITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: 03495.0227-00000
; CURRENT APPLICATION NUMBER: US/10/133,628
; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human NDPK-B: N1155
; OTHER INFORMATION: protein sequence
US-10-133-628-4
Query Match 99.4%; Score 798; DB 4; Length 152;
Best Local Similarity 99.3%; Pred. No. 5.4e-82;
Matches 151; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPLVKYMNKSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIVQGRNIHGS 120

Db 61 FPGLVKYMNSGPVVMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAKEISLWFKPELVDYKSCAHDWYVE 152
Db 121 DSVKSAKEISLWFKPELVDYKSCAHDWYVE 152

RESULT 9
US-10-732-923-13127
; Sequence 13127, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13127
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13127

Query Match 98.9%; Score 794; DB 5; Length 152;
Best Local Similarity 98.0%; Pred. No. 1.5e-81;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MANLRTFAIKPDGVORGVLGVEIIKRFQKGFRLVAMKFLRASEEHLKOHYIDLKDRPF 60
Db 1 MANLRTFAIKPDGVORGVLGVEIIKRFQKGFRLVAMKFLRASEEHLKOHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPVVMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPVVMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAKEISLWFKPELVDYKSCAHDWYVE 152
Db 121 DSVKSAKEISLWFKPELVDYKSCAHDWYVE 152

RESULT 10
US-10-363-829-352
; Sequence 352, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Iman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749

; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 352
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG:1098570.1.orf3:2000SEP08
US-10-363-829-352

Query Match 98.9%; Score 794; DB 4; Length 190;
Best Local Similarity 98.0%; Pred. No. 2e-81;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MANLRTFAIKPDGVORGVLGVEIIKRFQKGFRLVAMKFLRASEEHLKOHYIDLKDRPF 60
Db 39 MANLRTFAIKPDGVORGVLGVEIIKRFQKGFRLVAMKFLRASEEHLKOHYIDLKDRPF 98
Qy 61 FPGLVKYMNSGPVVMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 99 FPGLVKYMNSGPVVMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 158
Qy 121 DSVKSAKEISLWFKPELVDYKSCAHDWYVE 152
Db 159 DSVKSAKEISLWFKPELVDYKSCAHDWYVE 190

RESULT 11
US-09-791-118A-4
; Sequence 4, Application US/09791118A
; Patent No. US20020034741A1
; GENERAL INFORMATION:
; APPLICANT: Werner, Sabine
; APPLICANT: Braun, Susanne
; APPLICANT: Penzberg, Jorn-Peter
; APPLICANT: Goppelt, Andreas
; APPLICANT: Regenbogen, Johannes
; TITLE OF INVENTION: Use of polypeptides or nucleic acids
; TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or
; TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for
; TITLE OF INVENTION: the identification of pharmacologically
; FILE REFERENCE: 50125/012002
; CURRENT APPLICATION NUMBER: US/09/791,118A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/199,312
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: DE 100 08 330.7
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-118A-4

Query Match 98.8%; Score 793; DB 3; Length 152;
Best Local Similarity 98.0%; Pred. No. 2e-81;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
QY 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
DB 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVSAEKEIHLWFKPEELIDYKSCAHDWVYE 152

RESULT 12

US-10-116-275-332
; Sequence 332, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116, 275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 332
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mouse
US-10-116-275-332

Query Match 98.8%; Score 793; DB 4; Length 152;
Best Local Similarity 98.0%; Pred. No. 2e-81;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
QY 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
DB 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVSAEKEIHLWFKPEELIDYKSCAHDWVYE 152

RESULT 13

US-10-732-923-13113
; Sequence 13113, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732, 923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13113

; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-13113

Query Match 98.8%; Score 793; DB 5; Length 152;
Best Local Similarity 98.0%; Pred. No. 2e-81;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
QY 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
DB 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVSAEKEIHLWFKPEELIDYKSCAHDWVYE 152

RESULT 14

US-10-133-628-5
; Sequence 5, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
; APPLICANT: GALLOIS-MONTBRUN, SARAH
; APPLICANT: SCHNEIDER, BENOIT
; APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
; APPLICANT: DEVILLE-BONNE, DOMINIQUE
; APPLICANT: VERON, MICHEL
; TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG
; FILE REFERENCE: 03495.0227-00000
; CURRENT APPLICATION NUMBER: US/10/133,628
; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human NDPK-B;
; OTHER INFORMATION: L55H-N115S protein sequence
US-10-133-628-5

Query Match 98.5%; Score 791; DB 4; Length 152;
Best Local Similarity 98.7%; Pred. No. 3.3e-81;
Matches 150; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
QY 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
DB 61 PPGLVKYMNSGPVVMWVEGLNVVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 15

US-10-732-923-13128
; Sequence 13128, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C

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; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13128
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13128

Query Match      98.0%; Score 787; DB 5; Length 152;
Best Local Similarity 97.4%; Pred. No. 9.5e-81;
Matches 148; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVORGLVGEIIRPEQKGPRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVORGLVGEIIRPEQKGPRLVAMKFLRASEEHLKQHYIDLKDRPF 60

Qy 61 FPGLVKYMNSGPVVAMVWEGINVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Db 61 FPGLVKYMNSGPVVAMVWEGINVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120

Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 DSVESAEEKEICLWFKPEELIDYKSCAHDWVYE 152
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Search completed: December 16, 2005, 17:01:37
Job time : 108.547 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:39:14 ; Search time 6.69182 Seconds
(without alignments)
153.021 Million cell updates/sec

Title: US-10-074-694-5
Perfect score: 803
Sequence: 1 MANLERTFIAIKPDGVQRGL.....WFKPEELVDYKSCAHDWVYE 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	100.0	152	6	US-10-821-234-1577
2	720	89.7	152	6	US-10-878-556A-49
3	335.5	41.8	136	7	US-11-055-822-966
4	335.5	41.8	136	7	US-11-055-822-994
5	307	38.2	141	6	US-10-467-657-4110
6	78	9.7	428	6	US-10-763-712A-118
7	69.5	8.7	795	6	US-10-770-726-49
8	68.5	8.5	430	6	US-10-525-710-8
9	67.5	8.4	371	6	US-10-793-626-3294
10	67.5	8.4	2261	6	US-10-995-561-600
11	66	8.2	135	7	US-11-194-246-297
12	65.5	8.2	459	6	US-10-793-626-2666
13	65	8.1	230	6	US-10-793-626-3314
14	65	8.1	1152	7	US-11-055-822-308
15	63.5	7.9	204	6	US-10-793-626-412
16	63.5	7.9	204	6	US-10-793-626-1218
17	63	7.8	366	6	US-10-510-386-42
18	62.5	7.8	548	6	US-10-793-626-326
19	62.5	7.8	1162	6	US-10-451-375-3
20	62.5	7.8	1198	6	US-10-451-375-4
21	62.5	7.8	1437	7	US-11-074-176-96
22	62	7.7	1008	7	US-11-055-822-312
23	61.5	7.7	618	6	US-10-467-657-2758
24	61.5	7.7	618	6	US-10-467-657-2728
25	61	7.6	295	7	US-11-143-980-31

26	61	7.6	349	7	US-11-074-176-226	Sequence 226, App
27	60.5	7.5	428	6	US-10-793-626-2050	Sequence 2050, Ap
28	60	7.5	293	6	US-10-467-657-4834	Sequence 4834, Ap
29	60	7.5	393	6	US-10-485-517-316	Sequence 316, App
30	59.5	7.4	110	7	US-11-053-076-190	Sequence 190, App
31	59.5	7.4	235	7	US-11-074-176-240	Sequence 240, App
32	59.5	7.4	1067	7	US/11/062	Sequence 3, Appli
33	59.5	7.4	1092	7	US/11/062	Sequence 6, Appli
34	59	7.3	347	6	US-10-467-657-6092	Sequence 6092, Ap
35	59	7.3	347	6	US-10-467-657-7548	Sequence 7548, Ap
36	59	7.3	1302	7	US-11-090-439-42	Sequence 42, Appl
37	58.5	7.3	890	6	US-10-510-386-26	Sequence 26, Appl
38	58	7.2	245	6	US-10-793-626-1658	Sequence 1658, Ap
39	58	7.2	348	6	US-10-467-657-8200	Sequence 8200, Ap
40	58	7.2	451	6	US-10-793-626-318	Sequence 318, App
41	58	7.2	1071	6	US-10-467-657-1654	Sequence 1654, Ap
42	58	7.2	1144	6	US-10-467-657-1820	Sequence 1820, Ap
43	57.5	7.2	206	6	US-10-467-657-524	Sequence 524, App
44	57.5	7.2	697	6	US-10-485-517-202	Sequence 202, App
45	57	7.1	266	6	US-10-793-626-2066	Sequence 2066, Ap

ALIGNMENTS

RESULT 1
US-10-821-234-1577
; Sequence 1577, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1577
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1577

Query Match	100.0%	Score	803	DB	6	Length	152
Best Local Similarity	100.0%	Pred. No.	1.1e-78				
Matches	152	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MANLERTFIAIKPDGVQRGLVGEIIRKFEQGRFLVAMKFLRASSEHLKQHYIDLKDRPF	60				
Db	1	MANLERTFIAIKPDGVQRGLVGEIIRKFEQGRFLVAMKFLRASSEHLKQHYIDLKDRPF	60				
Qy	61	FPGLVKYMNSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIHGS	120				
Db	61	FPGLVKYMNSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIHGS	120				
Qy	121	DSVKSAREKISLWFKPEELVDYKSCAHDWVYE	152				
Db	121	DSVKSAREKISLWFKPEELVDYKSCAHDWVYE	152				
RESULT 2							
US-10-878-556A-49							
; Sequence 49, Application US/10878556A							
; Publication No. US20050266399A1							
; GENERAL INFORMATION:							
; APPLICANT: Hoffmann La-Roche Inc.							
; TITLE OF INVENTION: HCV regulated protein expression							
; FILE REFERENCE: 21762							

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; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 49
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ndka_human
; DATABASE ENTRY DATE: 1990-04-01
US-10-878-556A-49

Query Match      89.7%; Score 720; DB 6; Length 152;
Best Local Similarity 88.2%; Pred. No. 7.5e-70;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQVQGLVGEIIRKPEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANCERTFIAIKPDGVQVQGLVGEIIRKPEQKGFRLVGLKFMQASEDLKQHYVDLDRPF 60
Qy 61 PGLVLYKYNNSGPVVAMVWEGVLNVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FAGLVKYNHSGPVVAMVWEGVLNVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPELVVDYKSCAHDWYVE 152
Db 121 DSVESAKEEIGLWFPHELVDYTSCAQNWIYE 152

RESULT 3
US-11-055-822-966
; Sequence 966, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 966
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-966
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Query Match      41.8%; Score 335.5; DB 7; Length 136;
Best Local Similarity 50.4%; Pred. No. 4.8e-29;
Matches 66; Conservative 23; Mismatches 41; Indels 1; Gaps 1;

Qy 5 ERTFIAIKPDGVQVQGLVGEIIRKPEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFPGL 64
Db 3 ERTLILIKPDGVNTNGHVGEIIRKPEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFPGL 62
Qy 65 VKYMNNSGPVVAMVWEGVLNVKTRVLMGETNP-ADSKPGTIRGDFCIQVGRNIHGS 123
Db 63 VEFITSAPLIAGIVGGERADAMWQLAGGTFPVAKATPGTIRGDFALTGVGVNHHGSDSP 122
Qy 124 KSAEKEISLWF 134
Db 123 ESAEREISLWF 133

RESULT 4
US-11-055-822-994
; Sequence 994, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 994
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-994

Query Match      41.8%; Score 335.5; DB 7; Length 136;
Best Local Similarity 50.4%; Pred. No. 4.8e-29;
Matches 66; Conservative 23; Mismatches 41; Indels 1; Gaps 1;

Qy 5 ERTFIAIKPDGVQVQGLVGEIIRKPEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFPGL 64
Db 3 ERTLILIKPDGVNTNGHVGEIIRKPEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFPGL 62
Qy 65 VKYMNNSGPVVAMVWEGVLNVKTRVLMGETNP-ADSKPGTIRGDFCIQVGRNIHGS 123
Db 63 VEFITSAPLIAGIVGGERADAMWQLAGGTFPVAKATPGTIRGDFALTGVGVNHHGSDSP 122
Qy 124 KSAEKEISLWF 134
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APPLICANT: Harnet, Stetan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Sulphur (mety)
FILE REFERENCE: 13111-00006-US
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009453

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; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 082.7
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-525-710-8

Query Match      8.5%; Score 68.5; DB 6; Length 430;
Best Local Similarity 22.4%; Pred. No. 4.9;
Matches 33; Conservative 15; Mismatches 46; Indels 53; Gaps 6;

QY 21 VGEIIRKFEQ-----KGRFLVAMKFLRASE-----EHLKQH-----YIDLKDRPFPFG 63
DB 273 MGAISPFNSFLLLQGLTLLHLMRHSENAYKVAEFLEQHQAVESVSYGLPSHPSYPL 332
QY 64 LVKTMNSGPPVVMWEGLVNVTGRVMLGE-----TNPADSK-----100
DB 333 AKYLPKGOAALTFFVKGVGVEAGKLIHSHVQLPSHLANVGDSKSLIIHPASTTHQOLSE 392
QY 101 -----FCTIRGDFCIOVGRNIH 118
DB 393 AEQRDAGVTGCMIR----LSVGTESI 415

RESULT 9
US-10-793-626-3294
; Sequence 3294, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3294
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3294

Query Match      8.4%; Score 67.5; DB 6; Length 371;
Best Local Similarity 21.9%; Pred. No. 5.2;
Matches 35; Conservative 25; Mismatches 45; Indels 55; Gaps 7;

QY 3 NLETFETAIRP-----DGVQRGL-----VGB-----IIRK-PEOKGF 33
DB 88 SLGXSVDVFPLLGPNGEDTIOGLFVELDIPVGVNGVLAASSMDKLVNKKQLFEHRL 147
QY 34 -RLVAMKFLRASEEHKQHYIDL-KDRPFPFGLVKYMNSGPPVA-----75
DB 148 POLPYISFLRSEYEKYENNIILKLVNDKLTYPVFVKPANLSSGVISKCNNEELKSGIAE 207
QY 76 -----MWEGLVNVTGRVMLGETNPADSKPGTIRGD 107
DB 208 AFQFDRKLVIIEQGINAREIEVAVLGNIDYPETTWPGEVVKD 247

RESULT 10
US-10-995-561-600
; Sequence 600, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 600
; LENGTH: 2261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-600

Query Match      8.4%; Score 67.5; DB 6; Length 2261;
Best Local Similarity 23.5%; Pred. No. 52;
Matches 20; Conservative 20; Mismatches 40; Indels 5; Gaps 3;

QY 13 PDGVQRGLVGEIIRKFEQGRFLVAMKFLRASEEHKQHYIDLKDRPFPFGLVKYMNSGP 72
DB 312 PEG--GGLKIKSLNWYEDNNYK--ALFGGNGTDEDAETFY-DNSTTPYCNDLMKNLESSP 366
QY 73 VVAMVWEGLVNVTGRVMLGETNPA 97
DB 367 LSRIIWKALKPLLVGKILYTPDTPA 391

RESULT 11
US-11-194-246-297
; Sequence 297, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Avidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592-US1 (W&R 268, 05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 297
; LENGTH: 135
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-297

Query Match      8.2%; Score 66; DB 7; Length 135;
Best Local Similarity 22.5%; Pred. No. 2.1;
Matches 23; Conservative 17; Mismatches 34; Indels 28; Gaps 3;

QY 39 KFL-----RASEEHLKQHYIDLKDRPFPFG-----LVKYMNSGPPVAMVWE-- 79
DB 28 KFLYEKSKTAKQKQKQVQVKEIKFRPGTDEGDYQVVKLSRLIFLEDGDKAKITVFR 87
QY 80 -----GLNVYKTRVMLGETNPADSKPGTIRGDFCIOV 112
DB 88 GREMAHQDGLDVLIERVKNDLAISVVSAPGKLEGRQAVV 129

RESULT 12
US-10-793-626-2666
; Sequence 2666, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
```

```
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2666
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2666

Query Match      8.2%; Score 65.5; DB 6; Length 459;
Best Local Similarity 26.9%; Pred. No. 11;
Matches 32; Conservative 16; Mismatches 54; Indels 17; Gaps 5;

Qy 8 FIAIKPDQVQRLVGEIIRFEQK-----GFRIVAMKFLRAS--EHLKQHYIDLKDR 58
Db 85 FFIIVGSLMKPNISNIGRLYPENDVMDAGFVIFYSVVMGALVSPILIQHYIDIRN- 143
Qy 59 PFFPGLVKYMSGPPVAMVWEGNLNVKT-GRVMLGETNPADS-----KPGTIRGDFCIQV 112
Db 144 --PHGGFLIAAIGMALGLVWYLLFNKRTLSIGMKPTNPLSSSEKKKYGTIIGIWIAT 200

RESULT 13
US-10-793-626-3314
; Sequence 3314, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3314
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3314

Query Match      8.1%; Score 65; DB 6; Length 230;
Best Local Similarity 23.6%; Pred. No. 5.2;
Matches 25; Conservative 16; Mismatches 39; Indels 26; Gaps 3;

Qy 28 FEQKGF-RLVAMKFLRASEHLKQHYIDL-KDRPFPGLVKYMSGPPVA----- 75
Db 10 FEHRLPQLPITSFISRYEYKYNIIKLVDNKLTPVFPKPNALNGSSVGISKCNNEEL 69
Qy 76 -----MVWEGNLNVKTRVMLGETNPADS-KPGTIRGD 107
Db 70 KSGIAEAFQFDRKLVEIQGINAREIEAVLGNDYPTETTPGEVVKD 115

RESULT 14
US-11-055-822-308
; Sequence 308, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
```

```
; APPLICANT: Zelder, Oskar
; APPLICANT: Habetherauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 308
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-308

Query Match      8.1%; Score 65; DB 7; Length 1152;
Best Local Similarity 24.6%; Pred. No. 41;
Matches 32; Conservative 21; Mismatches 53; Indels 24; Gaps 7;

Qy 16 VQRG-LVGEIIRFEQKGFRLVAMKFLRASBEHLKQHYI-DLKDRPFPGLVKYMSGPPV 73
Db 93 IQAGSLVGRALPQ-----VVVPAARARTRQWGHMIVDARDKQFAKAVAEIQSDG-- 142
Qy 74 VAMVWEGNLNVKTRVMLGETNPADS-KPGTIRGDFCIQVGRNIHGSOSVSKAEKEISLW 133
Db 143 -----HRLNINLGEAVLGRKEAAKHLDDTVR-----LLRRPDVEYVSIKSSVASQISMW 193
Qy 134 -FKPEELVDY 142
Db 194 GF--EDTVNY 201

RESULT 15
US-10-793-626-412
; Sequence 412, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 412
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
```

US-10-793-626-412

```
Query Match      7.9%; Score 63.5; DB 6; Length 204;
Best Local Similarity 21.4%; Pred. No. 6.4;
Matches 25; Conservative 20; Mismatches 41; Indels 31; Gaps 3;

Qy      24 IIRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRP-----F 60
      :|||: : : : : : : : : : : : : : : : : :
Db      76 MLKRFKIETLFFVIVMSLSSTLNPLLNIPD-RERPTLLRLIDISGFSPFGHAMGSTSF 134

Qy      61 FPGLVKYN-----SGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCI 110
      : : : : : : : : : : : : : : : : : :
Db     135 FGSAYVINRRHDSGISKVLIGLCALFILLISTSRVYLGVRHYPTDIIAGIIGGVFCL 191
```

Search completed: December 16, 2005, 17:01:58
Job time : 7.69182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:59 ; Search time 138.333 Seconds
(without alignments)
527.255 Million cell updates/sec

Title: US-10-074-694-3

Perfect score: 876

Sequence: 1 QSQPAVKPCHLKGTMANSEK.....WFOPELVELVKSCAQNWYE 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	798	91.1	152	4	AAG80281 Murine NM
2	795	90.8	223	4	AAM78984 Human pro
3	794	90.6	178	5	AAM69421 Lung smal
4	794	90.6	180	9	AEA90110 Human NM2
5	794	90.6	180	9	AEAB8772 Human NM2
6	794	90.6	183	3	AAB14823 Human NM2
7	794	90.6	184	5	AAO26422 Protein o
8	794	90.6	184	5	AAG79335 Human NM2
9	774.5	88.4	177	5	AAE21724 Human PKI
10	764	87.2	153	8	ADR66938 Human pro
11	764	87.2	153	8	ADR66040 Human pro
12	761.5	86.9	177	5	ABB99909 Nucleotid
13	759	86.6	152	2	AAAR11903 Human NM2
14	759	86.6	152	2	AAW62505 Human NM2
15	759	86.6	152	5	AAG79338 Mature hu
16	759	86.6	152	7	ADF76437 Novel hum
17	759	86.6	152	8	ADL82817 Human PRO
18	759	86.6	152	8	ADN05777 Antipsori
19	759	86.6	152	8	ADO19200 Human PRO
20	759	86.6	152	8	ABM81903 Tumour-as
21	759	86.6	152	8	ADP54261 Human PRO
22	759	86.6	152	8	ADP23235 PRO polyp
23	759	86.6	152	8	ADU06448 Novel bro
24	759	86.6	152	9	ADW08712 Human pro

25	759	86.6	152	9	ADX05642	Adx05642 Cyclin-de
26	759	86.6	152	9	ADY19471	Ady19471 PRO polyp
27	759	86.6	152	9	ADY14586	Ady14586 PRO polyp
28	759	86.6	152	9	ADY81119	Ady81119 Human bra
29	759	86.6	152	9	AEI11912	Aeb11912 Human NM2
30	755	86.2	152	4	AAE60680	Aab60680 Bovine nu
31	754	86.1	152	4	AAE60681	Aab60681 Bovine nu
32	734	83.8	176	3	AAI14812	Aab14812 Human NM2
33	734	83.8	176	5	AAO26423	Aao26423 Protein o
34	734	83.8	176	5	AAO26423	Aao26423 Protein o
35	733	83.7	152	4	AAG80280	Ag80280 Human NM2
36	729	83.2	152	2	AAO70000	Aay07000 mm23-H2 p
37	729	83.2	152	4	AAG80282	Ag80282 Human NM2
38	729	83.2	152	5	AAG79337	Ag79337 Mature hu
39	729	83.2	152	6	ABU89707	Abu89707 Protein d
40	729	83.2	152	8	ADH17091	Adh17091 Human nm2
41	729	83.2	152	8	ABM81902	Abm81902 Tumour-as
42	729	83.2	152	8	ADP23162	Adp23162 PRO polyp
43	729	83.2	152	9	ADX05640	Adx05640 Cyclin-de
44	729	83.2	152	9	ADY14458	Ady14458 PRO polyp
45	729	83.2	152	9	ADY19693	Ady19693 PRO polyp

ALIGNMENTS

RESULT 1

AAG80281

ID AAG80281 standard; protein; 152 AA.

XX AAG80281;

AC AAG80281;

XX AAG80281;

DT 12-FEB-2002 (first entry)

XX AAG80281;

DE Murine NM23A protein.

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

XX AAG80281;

CC GTPases. The proteins of the invention, antibodies (Ab) directed against
CC them, and their encoding nucleic acids, or related vectors, transformed
CC cells and antisense sequences, are used for analysis, diagnosis,
CC prevention and/or treatment of skin and intestinal diseases (where
CC associated with uncontrolled tissue growth or cell differentiation,
CC particularly skin and intestinal tumours, also psoriasis, Crohn's disease
CC and ulcers), wound healing and/or associated pathological alterations).
CC They are also used to screen for agents that are potentially useful for
CC treating these conditions. In vitro monitoring of NM23 protein expression
CC in tissue samples provides an early diagnosis of disease. This sequence
CC represents the murine NM23A protein described in the method of the
CC invention
CC
XX
SQ Sequence 152 AA;

Query Match 91.1%; Score 798; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 38-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60

QY 75 FTGLVKYMHSGPPVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
Db 61 FTGLVKYMHSGPPVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120

QY 135 DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 166
Db 121 DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 152

RESULT 2
AAU78984
ID AAM78984 standard; protein; 223 AA.

AC AAM78984;
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1646.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
DR N-PSDB; AAKS2117.
XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 3984; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 223 AA;

Query Match 90.8%; Score 795; DB 4; Length 223;
Best Local Similarity 91.5%; Pred. No. 1.1e-81;
Matches 150; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 QPAVKPCHLGTMANSERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDL 62
Db 60 QPEFPKQLEGTMANCERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDL 119

QY 63 KEHYTDLKDRPFPTGLVKYMHSGPPVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDF 122
Db 120 KEHYTDLKDRPFPAFLVKYMHSGPPVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDF 179

QY 123 CIQVGRNIIHGS DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 166
Db 180 CIQVGRNIIHGS DSVKSAEKEISLWFOPEELVDYTSACQNIWE 223

RESULT 3
AAU69421
ID AAU69421 standard; protein; 178 AA.
XX
XX AAU69421;
XX
DT 30-JAN-2002 (first entry)
XX
XX Lung small cell carcinoma antigen #15.
DE
XX Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
KW lung cancer.
XX
XX Homo sapiens.
XX
XX WO200177168-A2.
XX
XX 18-OCT-2001.
XX
XX 11-APR-2001; 2001WO-US011859.
XX
XX 11-APR-2000; 2000US-0196780P.
XX
XX 21-JUN-2000; 2000US-0213361P.
XX
XX 01-SEP-2000; 2000US-0229763P.
XX
XX 05-SEP-2000; 2000US-0230629P.
XX
XX 14-SEP-2000; 2000US-0232565P.
XX
XX 19-DEC-2000; 2000US-0257037P.
XX
XX 08-JAN-2001; 2001US-0260796P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Lodes MJ, Wang T, Mohamath R, Indirias CY;
XX WPI; 2002-010896/01.
DR N-PSDB; AAS61861.

XX Lung tumor polynucleotide and polypeptides useful in therapy and
PT diagnosis of cancer especially lung cancer.
XX
XX Claim 2; Page 282; 295pp; English.
XX
CC The invention relates to novel isolated lung small cell cancer antigen
CC polynucleotides (I) and polypeptides (II) used in a method of detecting
CC cancer in a patient. The method is optionally performed by utilizing
CC oligonucleotides (III), where the biological sample from the patient is
CC contacted with (III), detecting the amount of polynucleotide hybridized
CC to (III) in the sample and comparing the amount of polynucleotide to a
CC predetermined cut-off value and thereby determining cancer in a patient.
CC (I), (II) or antigen-presenting cells expressing (II) is useful for
CC stimulating and/or expanding T cells specific for a tumor protein. The
CC method comprises contacting T cells with one of the components under
CC conditions to permit the stimulation and/or expansion of the cells. A
CC composition comprising (I) is useful for stimulating an immune response
CC in a patient and for inhibiting the development of a cancer especially
CC lung cancer in a patient. An isolated T cell population is useful for
CC removing tumour cells from the biological sample and for inhibiting the
CC development of cancer in a patient. AAU69407-AAU69431 represent novel
CC human lung small cell cancer antigen amino acid sequences of the
CC invention
XX
SQ Sequence 178 AA;

Query Match 90.6%; Score 794; DB 5; Length 178;
Best Local Similarity 91.5%; Pred. No. 1.1e-81;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 QPAVKPCHLKGTMANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 62
DB 15 QPEFKPKQLEGTMANCERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 74

QY 63 KEHYTDLKDRPFTGLVKYMHSGPVVAMVWEGNLVVKTRVMLGETNPADSKPGTIRGDF 122
DB 75 KEHYVDLKDPPFPAGLVKYMHSQPVVAMVWEGNLVVKTRVMLGETNPADSKPGTIRGDF 134

QY 123 CIOVGRNIHGSQSVSAEKEISLWFOPEELVEYKSCAQNIWE 166
DB 135 CIOVGRNIHGSQSVSAEKEISLWFOPEELVEYKSCAQNIWE 178

RESULT 4
AEA90110
ID AEA90110 standard; protein; 180 AA.
AC AEA90110;
XX
XX 25-AUG-2005 (first entry)
XX
XX Human NM23 protein, SEQ ID NO: 2.
DE Selectable marker; screening; diagnosis; liver disease; hepatotropic;
XX gastrointestinal disease; liver cirrhosis; liver cancer; cytostatic;
KW neoplasm; antigen; NM23 protein.
XX
OS Homo sapiens.
XX
XX US2005136489-A1.
XX
XX 23-JUN-2005.
XX
XX 17-DEC-2004; 2004US-00013684.
XX
XX 19-DEC-2003; 2003TW-00136309.
XX
XX (INTE-) IND TECHNOLOGY RES INST.
XX
XX Tseng T, Cheng P;
XX
XX WPI; 2005-444137/45.
DR

DR EMBL; CAA35621.
XX
XX New biomarker for liver diseases comprising specific sequences, useful
PT for developing kits for diagnosing liver cirrhosis or liver cancer.
XX
XX Claim 1; SEQ ID NO 2; 40pp; English.
XX
CC The invention relates to novel biomarkers for liver diseases. The
CC invention also relates to the use of an autoantigen screening method to
CC identify biomarkers that can be used in detecting liver diseases such as
CC liver cirrhosis and liver cancer. The present sequence is the human NM23
CC protein. This sequence is the autoantigen identified from cell lines
CC using sera of patients with liver cirrhosis and liver cancer.
XX
SQ Sequence 180 AA;

Query Match 90.6%; Score 794; DB 9; Length 180;
Best Local Similarity 91.5%; Pred. No. 1.1e-81;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 QPAVKPCHLKGTMANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 62
DB 17 QPEFKPKQLEGTMANCERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 76

QY 63 KEHYTDLKDRPFTGLVKYMHSGPVVAMVWEGNLVVKTRVMLGETNPADSKPGTIRGDF 122
DB 77 KEHYVDLKDPPFPAGLVKYMHSQPVVAMVWEGNLVVKTRVMLGETNPADSKPGTIRGDF 136

QY 123 CIOVGRNIHGSQSVSAEKEISLWFOPEELVEYKSCAQNIWE 166
DB 137 CIOVGRNIHGSQSVSAEKEISLWFOPEELVEYKSCAQNIWE 180

RESULT 5
AEB87772
ID AEB87772 standard; protein; 180 AA.
XX
XX AEB87772;
XX
XX 06-OCT-2005 (first entry)
XX
XX Human NM23, breast tumor marker.
XX
XX Breast tumor; breast disease; endocrine disease;
KW gynecology and obstetrics; neoplasm; prognosis; tumor marker;
KW DNA library; microarray; expression; NM23.
XX
XX Homo sapiens.
XX
XX WO2005071419-A2.
XX
XX 04-AUG-2005.
XX
XX 17-JAN-2005; 2005WO-18000261.
XX
XX 16-JAN-2004; 2004US-0537412P.
PR 14-JAN-2005; 2005US-00036298.
XX
XX (IPSO-) IPSOGEN.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES.
XX
XX Jacquemier J, Bertucci F, Birnbaum D, Debono S, Tagett R;
XX
XX WPI; 2005-564257/57.
XX
XX Analyzing differential protein expression associated with histopathologic
PT features of breast disease, comprises detecting overexpression or
PT underexpression of pool of proteins having Afadin, Aurora A, in breast
PT tissues or cells.
XX
XX Disclosure; SEQ ID NO 42; 87pp; English.
PS
XX

CC The present invention provides a method for analyzing differential
 CC protein expression associated with histopathological features of breast
 CC disease, in particular breast tumors, e.g. breast carcinomas, comprising
 CC detecting the overexpression or underexpression of a pool of proteins in
 CC breast tissues or cells. The pool comprises all or part of a protein set
 CC comprising: afadin, aurora A, alpha-catenin, beta-catenin, BCL2, cyclin
 CC D1, cyclin E, cytokeratin 5/6, cytokeratin 8/18, E-cadherin, EGFR, ERBB2,
 CC ERBB3, ERBB4, estrogen receptor, FGFR1, FHIT, GATA3, K167, mucin 1, p53,
 CC P-cadherin, progesterone receptor, TACC1, TACC2, TACC3, cytokeratin 6,
 CC cytokeratin 18, angi, aurora B, BCRP1, cathepsin D, CD10, CD44, CK14,
 CC cox2, fibroblast growth factor 2 (FGF2), GATA4, hifa, matrix
 CC metalloproteinase (MMP) 9, MTA1, NM23, neurogulins (NRG) 1 alpha, NRG1
 CC beta, p27, parkin, PLAU, S100, SCRIBBLE, smooth muscle actin,
 CC thrombospondin (THBS) 1, tissue-inhibitors of matrix metalloprotease 1
 CC (TIMP1). The measuring of over- or underexpression of proteins is carried
 CC out on tissue microarray, by immunohistochemistry (IHC) technologies. The
 CC method may involve comparing expression levels of the protein set in a
 CC control sample to levels of equivalent proteins in a tissue sample. The
 CC detection may also involve detecting the over- or underexpression of
 CC nucleic acids coding for the proteins. Also claimed are a protein library
 CC and a nucleic acid library useful for the molecular characterization of
 CC histopathological features of breast disease. The method is useful for
 CC analyzing differential protein expression associated with
 CC histopathological features of breast disease. It is also useful for
 CC detecting, diagnosing, staging, monitoring, predicting, and preventing
 CC conditions associated with breast cancer, predicting clinical outcome of
 CC breast cancer, predicting occurrence of metastatic relapse, and for
 CC determining the stage or aggressiveness of a breast cancer. Treatment of
 CC a patient can be based on the analysis of the differential protein
 CC expression profile. Breast cancers can be classified into prognostically
 CC relevant subclasses, and appropriate doses and/or schedule of
 CC chemotherapeutics and/or biopharmaceuticals and/or radiation therapy can
 CC be selected to circumvent toxicities in a patient. The method is also
 CC useful in assessing breast cancer heterogeneity and prognosis in patients
 CC with stage I, II or III disease. The present sequence is that of NM23.
 CC
 XX Sequence 180 AA;

Query Match 90.6%; Score 794; DB 9; Length 180;
 Best Local Similarity 91.5%; Pred. No. 1.1e-81;
 Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 QPAVKPCHLKGTWANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 62
 DB 17 QPEFKPKQLEGTMANCERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 76
 QY 63 KEHYTDLKDPRPFTGLVKYMHSGPVVAMVWEGVLNVVKTGRVMLGETNPADSKPGTIRGDF 122
 DB 77 KEHYVDLKDPRPFPAGLVKYMHSVPVAMVWEGVLNVVKTGRVMLGETNPADSKPGTIRGDF 136
 QY 123 CIQVGRNIHSGDSVKSAEKISLWFQPEELVEYKSCAQNIWE 166
 DB 137 CIQVGRNIHSGDSVKSAEKISLWFHPEELVDYTSACQNIWE 180

RESULT 6
 AAB14823

ID AAB14823 standard; protein; 183 AA.

XX

AC AAB14823;

XX 19-DEC-2000 (first entry)

DT

XX Human nm23 protein nm23-H1.

DE

XX Human; nm23-H1; tumour metastasis; cancer susceptibility;

KW chromosome 17q21.

KX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT Misc-difference 1

FT /note= "encoded by CGG"

FT Misc-difference 33 /note= "putative first amino acid"

FT

XX

FN US6087117-A.

XX

PD 11-JUL-2000.

XX

PF 07-JUN-1995; 95US-00475684.

XX

PR 18-OCT-1989; 89US-00422801.

PR

11-DEC-1991; 91US-00806932.

XX

(USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Liotta LA, Steeg PS, King CR;

XX

DR WPI; 2000-531342/48.

DR

N-PSDB; AAA70316.

XX

PT New nm23 monoclonal antibody which recognizes human nm23 protein, useful

PT

for detecting tumors which have low levels of nm23 protein and thus an

PT

increased ability to metastasize or be malignant.

XX

PS Claim 1; Fig 6; 21pp; English.

XX

CC The present sequence is the human nm23 protein nm23-H1, the gene for
 CC which is found on chromosome 17q21. Its coding sequence was isolated by
 CC searching a human fibroblast cDNA library for sequences similar to pm23-
 CC M1. Nm23 proteins are involved in tumour metastasis, and this protein,
 CC its gene and antibodies can be used to determine an individual's
 CC susceptibility to cancer and the likelihood of tumour metastasis within
 CC that individual. This is possible using a number of methods, including
 CC Northern blotting, nuclease protection assays, in situ hybridisation,
 CC immunohistochemical analysis and solid phase immunoassays

XX

SQ Sequence 183 AA;

Query Match 90.6%; Score 794; DB 3; Length 183;

Best Local Similarity 91.5%; Pred. No. 1.1e-81;

Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 QPAVKPCHLKGTWANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 62

DB 20 QQFKPKQLEGTMANCERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 79

QY 63 KEHYTDLKDPRPFTGLVKYMHSGPVVAMVWEGVLNVVKTGRVMLGETNPADSKPGTIRGDF 122

DB 80 KEHYVDLKDPRPFPAGLVKYMHSVPVAMVWEGVLNVVKTGRVMLGETNPADSKPGTIRGDF 139

QY 123 CIQVGRNIHSGDSVKSAEKISLWFQPEELVEYKSCAQNIWE 166

DB 140 CIQVGRNIHSGDSVKSAEKISLWFHPEELVDYTSACQNIWE 183

RESULT 7

AAO26422

ID AAO26422 standard; protein; 184 AA.

XX

AC AAO26422;

XX

DT 07-FEB-2003 (first entry)

XX

DE Protein of the nm23-H1 cDNA.

XX

XX Human nm23 protein; nm23-H1; nm23-H2S; cancer; malignant potential;

KW human tumour; genetic predisposition.

XX

OS Unidentified.

XX

FN US6423836-B1.

XX

PD 23-JUL-2002.

XX

Db 1 TMANCERTFAIKPDGVQVGLVGEIIKRFQKGRFLVGLKFMQASEDLLKHEHYVDLKD RP 60
QY 74 FFTGLVKYHSGPVMVWVGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHG 133
Db 61 FFAGLVKYHSGPVMVWVGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHG 120
QY 134 SDSVKSAEKISLWFOPEELVEYKSCAQNIYE 166
Db 121 SDSVSAEKEIGLWFFPEELVDVTSQAQNIYE 153

RESULT 11
ADR66040
ID ADR66040 standard; protein; 153 AA.
XX
AC ADR66040;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived protein SEQ ID 236 #1.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
XX WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 2; Page 631; 1607pp; German.
XX

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from

CC prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; CC biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The CC samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and CC lymph node metastases were also stained. ADR6905-ADR6954 represent the CC polynucleotide and polypeptide sequences used in the method of the CC invention.
XX
SQ Sequence 153 AA;
Query Match 87.2%; Score 764; DB 8; Length 153;
Best Local Similarity 94.1%; Pred. No. 2.2e-78;
Matches 144; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 14 TMANCERTFAIKPDGVQVGLVGEIIKRFQKGRFLVGLKFMQASEDLLKHEHYVDLKD RP 73
Db 1 TMANCERTFAIKPDGVQVGLVGEIIKRFQKGRFLVGLKFMQASEDLLKHEHYVDLKD RP 60
QY 74 FFTGLVKYHSGPVMVWVGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHG 133
Db 61 FFAGLVKYHSGPVMVWVGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHG 120
QY 134 SDSVKSAEKISLWFOPEELVEYKSCAQNIYE 166
Db 121 SDSVSAEKEIGLWFFPEELVDVTSQAQNIYE 153

RESULT 12
ABB99909
ID ABB99909 standard; protein; 177 AA.
XX
AC ABB99909;
XX
DT 24-JAN-2003 (first entry)
XX
DE Nucleotide diphosphate kinase 19.47.
XX
KW Nucleotide diphosphate kinase 19.47; recombinant production;
KW gene therapy; tumour; cancer; embryonic development disorder; paralysis;
KW cytosolic; enzyme.
XX
OS Unidentified.
XX
PN CN1351016-A.
XX
PD 29-MAY-2002.
XX
PF 26-OCT-2000; 2000CN-00125776.
XX
PR 26-OCT-2000; 2000CN-00125776.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-644397/70.
DR N-PSDB; ABQ77987.
XX
PT Polypeptide-protein 19.47 containing nucleoside diphosphate kinase
PT activity site characteristics and polynucleotide for encoding it.
XX
PS Claim 1; Page 27 (Disclosure); 33pp; Chinese.
XX

The invention relates to nucleoside diphosphate kinase 19.47 (ABB99909) and nucleic acids encoding it (ABQ77987). The protein has a molecular weight of 19.47 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. Nucleoside diphosphate kinase 19.47 can be used in the treatment of a variety of diseases such as tumours, embryonic development disorders and

D6 61 FAGLVKYMHSPPVAVMWEGINLVKTRVNLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
QY 135 DSVKSAKEISLWFOPELVEYKSCAQNWIYE 166
DB 121 DSVESAKEIGLWHPHELVDYTSQAQNWIYE 152

RESULT 15

AAG79338
ID AAG79338 standard; protein; 152 AA.
XX
AC AAG79338;
XX
DT 21-AUG-2002 (first entry)
XX
DE Mature human NM23-H1.
XX
KW NM23-H1; NM23-H2S; aggressiveness; metastatic potential; tumour;
KW cancer susceptibility; early-onset familial breast cancer.
XX
OS Homo sapiens.
XX
PN US6329198-B1.
XX
PD 11-DEC-2001.
XX
XX 18-JUN-1999; 99US-00335948.
XX
PR 18-OCT-1989; 89US-00422801.
PR 11-DEC-1991; 91US-00806932.
PR 07-JUN-1995; 95US-00475684.
XX
XX (USHE-) US DEPT SEC HEALTH & HUMAN SERVICES.
XX
PI King CR, Steeg PS, Liotta LA;
XX
DR WPI; 2002-121137/16.
DR N-PSDB; AAI72921.
XX
PT New human NM23 protein, useful for diagnosis and prognosis of cancer, and
PT assessment of aggressiveness and susceptibility.
XX
PS Claim 2; Col 21-24; 23pp; English.
XX
CC The sequences given in AAG79335-38 show the related human proteins NM23-
CC H1 and H2S. These proteins are products of different genes, with NM23-H1
CC being localised to chromosome 17. These proteins are used to predict
CC aggressiveness (metastatic potential) of human tumours and in genetic
CC tests for cancer susceptibility, diagnosis and prognosis, also for
CC selection of treatment, e.g. susceptibility to early-onset familial
CC breast cancer. Gene nm23 may contribute to tumourigenicity and alteration
CC in its regulation may be an early stage in the metastatic cascade.
CC Allelic or homozygous deletion of the gene is detected in some primary
CC tumour cells
XX
SQ Sequence 152 AA;

Query Match 86.6%; Score 759; DB 5; Length 152;
Best Local Similarity 94.1%; Pred. No. 8.3e-78;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 15 MANSERTFIAIKPDGVORGLVGEIIRKPEQKGRFLVGLKFLQASEDLKHEHYTLKDRPF 74
DB 1 MANSERTFIAIKPDGVORGLVGEIIRKPEQKGRFLVGLKFLQASEDLKHEHYTLKDRPF 60
QY 75 FTGLVKYMHSPPVAVMWEGINLVKTRVNLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
DB 61 FAGLVKYMHSPPVAVMWEGINLVKTRVNLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
QY 135 DSVKSAKEISLWFOPELVEYKSCAQNWIYE 166
DB 121 DSVESAKEIGLWHPHELVDYTSQAQNWIYE 152

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:59 ; Search time 24.5346 Seconds
(without alignments)
650.999 Million cell updates/sec

Title: US-10-074-694-3
Perfect score: 876
Sequence: 1 QSQPAVKPCHLKGTMANSR.....WFQPEELVEYKCAQNWYE 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	876	100.0	166	2 A46557	nucleoside-diphosp
2	779	88.9	152	2 A45208	nucleoside-diphosp
3	759	86.6	152	1 A33386	nucleoside-diphosp
4	729	83.2	152	2 A49798	nucleoside-diphosp
5	720	82.2	152	2 A38369	nucleoside-diphosp
6	719	82.1	152	2 S29241	nucleoside-diphosp
7	611	69.7	153	2 S01908	nucleoside-diphosp
8	547.5	62.5	168	2 I39074	nucleoside-diphosp
9	528.5	60.3	153	2 T21354	hypothetical prote
10	519.5	59.3	153	2 JC4359	nucleoside-diphosp
11	514.5	58.7	149	2 S33170	nucleoside-diphosp
12	514.5	58.7	238	2 T01877	nucleoside-diphosp
13	513	58.6	237	2 T08909	hypothetical prote
14	510.5	58.3	148	2 T14183	nucleoside-diphosp
15	510	58.2	154	2 T50459	nucleoside-diphosp
16	500.5	57.1	149	2 T07042	nucleoside-diphosp
17	499.5	57.0	148	2 S24165	nucleoside-diphosp
18	495.5	56.6	149	2 T17131	nucleoside-diphosp
19	494	56.4	153	2 S60363	nucleoside-diphosp
20	492	56.2	153	2 S37889	nucleoside-diphosp
21	491	56.1	151	1 T39099	nucleoside-diphosp
22	490.5	56.0	147	2 S31444	nucleoside-diphosp
23	487.5	55.7	149	2 S43330	nucleoside-diphosp
24	478	54.6	155	2 A49547	nucleoside-diphosp
25	476	54.3	149	2 S76467	nucleoside-diphosp
26	475.5	54.3	144	2 S47974	nucleoside-diphosp
27	472	53.9	231	2 T52586	nucleoside-diphosp
28	461	52.6	152	2 T51612	nucleoside-diphosp
29	460	52.5	220	2 B49547	nucleoside-diphosp

ALIGNMENTS

RESULT 1

A46557
nucleoside-diphosphate kinase (EC 2.7.4.6) - mouse (fragment)
N;Alternate names: differentiation-inhibiting factor; tumor metastasis inhibitor NM23
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence revision 03-Mar-1994 #text_change 05-Oct-2004
C;Accession: A46557; B33386; I52807; JN0281
R;Steeg, P.S.; Bevilacqua, G.; Kopper, L.; Thorgerisson, U.P.; Talmadge, J.E.; Liotta, L.
J. Natl. Cancer Inst. 80, 200-204, 1988
A;Title: Evidence for a novel gene associated with low tumor metastatic potential.
A;Reference number: A46557; MUID:88155671; PMID:3346912
A;Accession: A46557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166 <STE>
A;Cross-references: UNIPROT:P15532; UNIPARC:UPI0000016CF64; GB:M35970; NID:g200066; PTDN:P
A;Note: the authors translated the codon TGG for residue 163 as Tyr
R;Rougard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M.K.
Nature 342, 177-180, 1989
A;Title: Reduced Nm23/Avd protein in tumour metastasis and aberrant Drosophila developmer
A;Reference number: A33386; MUID:90044071; PMID:2508941
A;Accession: B33386
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 15-166 <ROS>
A;Cross-references: UNIPARC:UPI000000188F
R;Leone, A.; Flatow, U.; King, C.R.; Sandeen, M.A.; Margulies, I.M.; Liotta, L.A.; Steeg,
Cell 65, 25-35, 1991
A;Title: Reduced tumor incidence, metastatic potential, and cytokine responsiveness of m
A;Reference number: I52807; MUID:91191558; PMID:2013093
A;Accession: I52807
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 15-166 <RES>
A;Cross-references: UNIPARC:UPI000000188F; GB:M65037; NID:g200069; PTDN:AA63391.1; PID:G
R;Okabe-Kado, J.; Kasukabe, T.; Honma, Y.; Hayashi, M.; Henzel, W.J.; Hozumi, M.
Biochem. Biophys. Res. Commun. 182, 987-994, 1992
A;Title: Identity of a differentiation inhibiting factor for mouse myeloid leukemia cells
A;Reference number: JN0281; MUID:92171977; PMID:1311576
A;Accession: JN0281
A;Molecule type: protein
A;Residues: 19-21,23-25; 'M';54-55,'R';57-59,'E';61,63,'Q';'YI';78-98;100-103;105-113;115-
A;Cross-references: UNIPARC:UPI0000055EF8; UNIPARC:UPI000015759C; UNIPARC:UPI0000175709;
70E; UNIPARC:UPI000017570F; UNIPARC:UPI0000175710
A;Experimental source: myeloid leukemia cell
C;Comment: This factor is Nm23/nucleoside diphosphate kinase (EC 2.7.4.6) involved in tun
C;Genetics:
A;Gene: nm23
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; I
F;29-33/Region: ATP binding #status predicted
F;132/Active site: His (phosphohistidine intermediate) #status predicted

```
Query Match      100.0%; Score 876; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSPAVKPCHLKGTMANSTFIAIKPDGVQVGLVGEIIKRFQKGFRLVGLKFLQASED 60
Db 1 QSPAVKPCHLKGTMANSTFIAIKPDGVQVGLVGEIIKRFQKGFRLVGLKFLQASED 60

Qy 61 LKKEHYTDLKDRPFPTGLVKYMHSGPVVAMVWEGLVNVTGRVLMGTNPADSKPGTIRG 120
Db 61 LKKEHYTDLKDRPFPTGLVKYMHSGPVVAMVWEGLVNVTGRVLMGTNPADSKPGTIRG 120

Qy 121 DFClQVGRNIIHGS DSVKSAEKEISLWFQPEELVEYKSCAQNIWE 166
Db 121 DFClQVGRNIIHGS DSVKSAEKEISLWFQPEELVEYKSCAQNIWE 166

RESULT 2
A45208
nucleoside-diphosphate kinase (EC 2.7.4.6) isoform beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A45208
R;Shimada, N.; Ishikawa, N.; Munakata, Y.; Toda, T.; Watanabe, K.; Kimura, N.
J. Biol. Chem. 268, 2583-2589, 1993
A;Title: A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolation and characterization of the cDNA.
A;Reference number: A45208; MUID: 93155067; PMID: 8381409
A;Accession: A45208
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-152 <SHI>
A;Cross-references: UNIPROT:Q05982; UNIPARC:UPI000012FE91; GB:D13374; NID:G286231; PIDN:
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:124170)
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      88.9%; Score 779; DB 2; Length 152;
Best Local Similarity 96.7%; Pred. No. 6.4e-67;
Matches 147; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 15 MANSERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 60

Qy 75 FTGLVKYMHSGPVVAMVWEGLVNVTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FSLGLVKYMHSGPVVAMVWEGLVNVTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120

Qy 135 DSVKSAEKEISLWFQPEELVEYKSCAQNIWE 166
Db 121 DSVESA EKEISLWFQPEELVDYKSCAQNIWE 152

RESULT 3
A33386
nucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H1g - human
N;Alternate names: nm23-H1g protein; probable metastasis suppressor nm23-H1
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A33386; S45376; A39838; A43931; A56882; B43931; C43931
R;Rosengard, A.M.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M.
Nature 342, 177-180, 1989
A;Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila development
A;Reference number: A33386; MUID: 90044071; PMID: 2509941
A;Accession: A33386
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-152 <ROS>
A;Cross-references: UNIPROT:P15531; UNIPARC:UPI0000112099; GB:X75598; NID:G468541; PIDN:
```

```
R;Dooley, S.; Seib, T.; Engel, M.; Theisinger, B.; Janz, H.; Piontek, K.; Zang, K.D.; Wej
Hum. Genet. 93, 63-66, 1994
A;Title: Isolation and characterization of the human genomic locus coding for the putativ
A;Reference number: S45376; MUID: 94095204; PMID: 8270257
A;Accession: S45376
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <DOO>
A;Cross-references: UNIPARC:UPI0000112099; EMBL:X75598; NID:G468541; PIDN:CAA53270.1; PII
R;Gilles, A.M.; Prescan, E.; Vonica, A.; Lascau, I.
J. Biol. Chem. 266, 8784-8789, 1991
A;Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characterizati
A;Reference number: A39838; MUID: 91224972; PMID: 1851158
A;Accession: A39838
A;Molecule type: protein
A;Residues: 1-152 <GIL>
A;Cross-references: UNIPARC:UPI0000112099
R;Hailat, N.; Keim, D.R.; Melhem, R.F.; Zhu, X.X.; Eckerskorn, C.; Brodeur, G.M.; Reynold
J. Clin. Invest. 88, 341-345, 1991
A;Title: High levels of p19/nm23 protein in neuroblastoma are associated with advanced st
A;Reference number: A43931; MUID: 91277302; PMID: 2056128
A;Accession: A43931
A;Molecule type: protein
A;Residues: 7-18;40-49;89-94 <HAI>
A;Cross-references: UNIPARC:UPI000004BCA0; UNIPARC:UPI00001726A4; UNIPARC:UPI00001726A5
A;Note: sequence modified after extraction from NCBI backbone
R;Wang, L.; Patel, U.; Ghosh, L.; Chen, H.C.; Banerjee, S.
Cancer Res. 53, 717-720, 1993
A;Title: Mutation in the nm23 gene is associated with metastasis in colorectal cancer.
A;Reference number: A56882; MUID: 93153759; PMID: 7916650
A;Accession: A56882
A;Molecule type: mRNA
A;Residues: 1-86, 'SAYKLAGTLYMAVILRWVRESACGFTLRN' <WAN>
A;Cross-references: UNIPARC:UPI00001726A6
A;Note: mutant sequence shown (tumor 10) was extracted from NCBI backbone; wild type seq.
C;Genetics:
A;Gene: GDB:NMEL1; nm23-H1
A;Cross-references: GDB:127965; OMIM:156490
A;Map position: 17q21-17q22
A;Introns: 43/1; 77/2; 114/2
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; blocked amino end; hexamer; phosphohistidine; phosphoprotein; p
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      86.6%; Score 759; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. No. 5.2e-65;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 15 MANSERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 60

Qy 75 FTGLVKYMHSGPVVAMVWEGLVNVTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FAGLVKYMHS GPVAMVWEGLVNVTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120

Qy 135 DSVKSAEKEISLWFQPEELVEYKSCAQNIWE 166
Db 121 DSVESA EKEISLWFHPEELVDYTSQAQNIWE 152

RESULT 4
A49798
nucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H2 - human
N;Alternate names: c-myc transcription factor PuF; tumor metastasis inhibitor nm23-H2
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 12-Mar-1999 #text_change 05-Oct-2004
C;Accession: A49798; B39838; I59581
R;Stahl, J.A.; Leone, A.; Rosengard, A.M.; Porter, L.; King, C.R.; Steeg, P.S.
Cancer Res. 51, 445-449, 1991
A;Title: Identification of a second human nm23 gene, nm23-H2.
```


A; Cross-references: UNIPARC:UPI000012FE93; GB:M55331; GB:J05588; NID:g205661; PIDN:AAA44
R; Ishikawa, N.; Shimada, N.; Munakata, Y.; Watanabe, K.; Kimura, N.
J. Biol. Chem. 267, 14366-14372, 1992

A; Title: Isolation and characterization of a gene encoding rat nucleoside diphosphate kinase
A; Reference number: A42967; MUID:92332552; PMID:1321145

A; Accession: A42967

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-152 <ISH>

A; Cross-references: UNIPARC:UPI000012FE93

A; Note: sequence extracted from NCBI backbone (NCBIN:108562, NCBIP:108564)

C; Superfamily: nucleoside diphosphate kinase

C; Keywords: Amp binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; P
F; 15-19/Region: ATP binding #status predicted

F; 118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 82.2%; Score 720; DB 2; Length 152;
Best Local Similarity 88.2%; Pred. No. 2.7e-61;
Matches 134; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 15 MANSERTIAIKPDGVQRGLVGEIIKRPEQGFRVLGKLPLOASEDLKKHYHTLKDORPF 74
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MANLERTIAIKPDGVQRGLVGEIIKRPEQGFRVLVAMKFRLASEEHLKHQHYIDLKDORPF 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 75 FTGLVKYMHSGPVAVMWEGNLNVKTGRVMLGETNPADSKPGTIRGDFCIQVGNRIHGS 134
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 FPGILVKYNNSGPVVAMWEGNLNVKTGRVMLGETNPADSKPGTIRGDFCIQVGNRIHGS 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 135 DSVSAEKELISLWFOPPELVVEYKSCAQNIYE 166
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 DSVESAEKEIGLWFKPPELDLYKCAHDWIYE 152
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6

S29241

Nucleoside-diphosphate kinase (EC 2.7.4.6) B - mouse

C; Species: Mus musculus (house mouse)

C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C; Accession: S29241

R; Urano, T.; Takamiya, K.; Furukawa, K.; Shiku, H.

FEBS Lett. 309, 359-362, 1992

A; Title: Molecular cloning and functional expression of the second mouse nm23/NDP kinase

A; Reference number: S29241; MUID:92387389; PMID:1325378

A; Accession: S29241

A; Molecule type: mRNA

A; Residues: 1-152 <URA>

A; Cross-references: UNIPROT:Q01768; UNIPARC:UPI000003EPD; EMBL:X68193; NID:g53353; PIDN:
C; Superfamily: nucleoside diphosphate kinase

C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; P
F; 15-19/Region: ATP binding #status predicted

F; 118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 82.1%; Score 719; DB 2; Length 152;
Best Local Similarity 88.2%; Pred. No. 3.3e-61;
Matches 134; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 15 MANSERTIAIKPDGVQRGLVGEIIKRPEQGFRVLGKLPLOASEDLKKHYHTLKDORPF 74
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MANLERTIAIKPDGVQRGLVGEIIKRPEQGFRVLVAMKFRLASEEHLKHQHYIDLKDORPF 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 75 FTGLVKYMHSGPVAVMWEGNLNVKTGRVMLGETNPADSKPGTIRGDFCIQVGNRIHGS 134
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 FPGILVKYNNSGPVVAMWEGNLNVKTGRVMLGETNPADSKPGTIRGDFCIQVGNRIHGS 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 135 DSVSAEKELISLWFOPPELVVEYKSCAQNIYE 166
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 DSVESAEKEIHLWFKPPELDLYKCAHDWIYE 152
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7

S01908

nucleoside-diphosphate kinase (EC 2.7.4.6) - fruit fly (*Drosophila melanogaster*)

N; Alternate names: K-pn protein; killer-of-prune protein

C;Species: Drosophila melanogaster
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S01908
R;Biggs, J.; Tripoulas, N.; Hersperger, E.; Dearolf, C.; Shearn, A.
Genes Dev. 2, 1333-1343, 1988
A;Title: Analysis of the lethal interaction between the prune and killer of prune mutants
A;Reference number: S01908; MUID:89079007; PMID:2849580
A;Accession: S01908
A;Molecule type: mRNA
A;Residues: 1-153 <BIG>
A;Cross-references: UNIPROT:P08879; UNIPARC:UPI00000011C4; EMBL:X13107; NID:G7634; PIDN:
C;Genetics:
A;Gene: awd
A;Cross-references: FlyBase:FBgn0000150
A;Map position: 3 100C-D
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;16-20/Region: ATP binding #status predicted
F;119/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 69.7%; Score 611; DB 2; Length 153;
Best Local Similarity 76.2%; Pred. No. 6.5e-51;
Matches 115; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 16 ANSERTFAIKPDGVQVGLVGEIIRPEQKGFRLVGLKFLQASEDLKHEHYTLKDRPPF 75
DB 3 ANKERTFIMVKPDGVQVGLVGEIIRPEQKGFRLVGLKFLQASEDLKHEHYTLKDRPPF 62
QY 76 TGLVKYMHSGPVVAMVWEGLVNVTGRVLMGTNPADSKFTGIRGDFCIQVGRNIIHGS 135
DB 63 PGLVNYMNSGPPVAMVWEGLVNVTGRVLMGTNPADSKFTGIRGDFCIQVGRNIIHGS 122
QY 136 SVKSAEKEISLWQPELVEYKSCAQNIWE 166
DB 123 AVESAKEIALWFEKELVTWTPAAKDWIYE 153

RESULT 8
I39074
nucleoside-diphosphate kinase (EC 2.7.4.6) DR-nm23 - human
N;Alternate names: DR-nm23 protein; non-metastatic cell-expressed protein 3
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: I39074
R;Venturelli, D.D.; Martinez, R.R.; Calabretta, B.B.
Proc. Natl. Acad. Sci. U.S.A. 92, 7435-7439, 1995
A;Title: Overexpression of DR-nm23, a protein encoded by a member of the nm23 gene famil
A;Reference number: I39074; MUID:95365382; PMID:7638209
A;Accession: I39074
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-168 <RES>
A;Cross-references: UNIPROT:Q13232; UNIPARC:UPI0000149FCF; EMBL:U29656; NID:G1051255; PI
C;Genetics:
A;Gene: GDB:NME3; DR-nm23
A;Cross-references: GDB:5215169; OMIM:601817
A;Map position: 16q13-16q13
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;32-36/Region: ATP binding #status predicted
F;134/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 62.5%; Score 547.5; DB 2; Length 168;
Best Local Similarity 66.2%; Pred. No. 8.1e-45;
Matches 98; Conservative 32; Mismatches 17; Indels 1; Gaps 1;

QY 19 ERTFIAIKPDGVQVGLVGEIIRPEQKGFRLVGLKFLQASEDLKHEHYTLKDRPPFTGL 78
DB 22 ERTFLAVKPDGVQVGLVGEIIRPERKGFRLVGLKFLQASEDLKHEHYTLKDRPPFTGL 81
QY 79 VKYMHSGPPVAMVWEGLVNVTGRVLMGTNPADSKFTGIRGDFCIQVGRNIIHGS 138
DB 82 VKYMASGPPVAMVWQGLDVVTRSRALIGATNPADAPPGTIRGDFCIQVGRNIIHGS 140

QY 139 SAEKEISLWQPELVEYKSCAQNIWE 166
DB 141 SARREIALWFRADLLCWEDSAGHWIYE 168

RESULT 9
T21354
hypothetical protein F25H2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21354
R;Wilkinson, J.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z19411
A;Accession: T21354
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-153 <WIL>
A;Cross-references: UNIPROT:Q93576; UNIPARC:UPI000007F609; EMBL:Z79754; PIDN:CAB02101.1;
A;Experimental source: clone F25H2
C;Genetics:
A;Gene: CESP:F25H2.5
A;Map position: 1
A;Introns: 18/2; 49/3
C;Superfamily: nucleoside diphosphate kinase

Query Match 60.3%; Score 528.5; DB 2; Length 153;
Best Local Similarity 65.4%; Pred. No. 4.6e-43;
Matches 100; Conservative 23; Mismatches 29; Indels 1; Gaps 1;

QY 15 MANSERTFAIKPDGVQVGLVGEIIRPEQKGFRLVGLKFLQASEDLKHEHYTLKDRPP 74
DB 1 MSNTERTFAIKPDGVHRLVGLVGEIIRPEQKGFRLVGLKFLQASEDLKHEHYTLKDRPP 60
QY 75 FTGLVKYMHSGPPVAMVWEGLVNVTGRVLMGTNPADSKFTGIRGDFCIQVGRNIIHGS 134
DB 61 FPSLIEYMSSGPPVAMVWQGLDVVKQGRSLGATNPALASAPGTIRGDFCIQVGRNIIHGS 120
QY 135 DSVKSAEKEISLWQPELVEYKS-CAQNIWE 166
DB 121 DAVDSANREIAHWFKOEINDYASPPINSWYE 153

RESULT 10
JC4359
nucleoside-diphosphate kinase (EC 2.7.4.6) - nematode (Brugia malayi)
C;Species: Brugia malayi
C;Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4359
R;Ghosh, I.; Raghavan, N.; FitzGerald, P.C.; Scott, A.L.
Gene 164, 261-266, 1995
A;Title: Nucleoside diphosphate kinase from the parasitic nematode Brugia malayi.
A;Reference number: JC4359; MUID:96069592; PMID:7590340
A;Accession: JC4359
A;Molecule type: mRNA
A;Residues: 1-153 <GHO>
A;Cross-references: UNIPROT:P48817; UNIPARC:UPI000012FE9C; GB:U18906; NID:G619942; PIDN:
C;Comment: This enzyme is a pivotal enzyme in the synthesis of nucleoside triphosphates c
de triphosphates, supplying GTP for GTP-binding proteins and a role in signal transductio
C;Genetics:
A;Gene: ndk
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; I
F;13-17/Region: ATP binding #status predicted
F;106/Active site: Arg #status predicted
F;119/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 59.3%; Score 519.5; DB 2; Length 153;
Best Local Similarity 62.7%; Pred. No. 3.3e-42;
Matches 96; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

QY 15 MANS-ERTFAIKPDGVQVGLVGEIIRPEQKGFRLVGLKFLQASEDLKHEHYTLKDRP 73

A;Experimental source: cultivar Columbia; BAC clone F25124

C;Genetics:

A;Gene: ATSP:F8M12.12; ATSP:F25124.220; ndpk3

A;Map position: 4

A;Introns: 28/1; 75/1; 87/3; 104/3; 160/3; 198/2

C;Superfamily: nucleoside diphosphate kinase

C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; I

F;99-103/Region: ATP binding #status predicted

F;123/Active site: Lys #status predicted

F;202/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 58.7%; Score 514; DB 2; Length 238;

Best Local Similarity 61.3%; Pred. No. 1.9e-41;

Matches 92; Conservative 27; Mismatches 31; Indels 0; Gaps 0;

QY 16 ANSERTFIAIKPDGVORGLVGBIIKRFQKGRLVGLKFLQASEDLLKEHYTDLKDRPFF 75
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
Db 86 AEWERTFIAIKPDGVORGLISIIISRFERKGFKLGIKVIVPSKDFQAQKHDLKERPFF 145
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
QY 76 TGLVKVMHSGPPVAMWVEGLNVVTKRVMLETNPADSKPGTIRGDFCIQVGRIIHGSD 135
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
Db 146 NGLCDPLSSGPVIAMWVEGDGVIRYRKILIGATDPQKSEPTIRGDLAVTVGNRIIHGSD 205
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
QY 136 SVKSAREKTSIWLFPQEELVEYKSCAQNIY 165
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
Db 206 GPETAKDEISLWFKPELVSYTSNKKWLY 235
| | | | | | | | | | | | | | | | | | | | : : : | | | | |

RESULT 13
T08909
hypothetical protein T32A16.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08909
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16518
A;Accession: T08909
A;Molecule type: DNA
A;Residues: 1-237 <BEV>
A;Cross-references: UNIPROT:O8LAH8; UNIPARC:UPI00000ABF3A; EMBL:AL078468; GSPDB:GN000062;
A;Experimental source: cultivar Columbia; BAC clone T32A16
C;Genetics:
A;Gene: ATSP:T32A16.70
A;Map position: 4
A;Introns: 28/1; 74/1; 86/3; 103/3; 159/3; 197/2
C;Superfamily: nucleoside diphosphate kinase

Query Match 58.6%; Score 513; DB 2; Length 237;
Best Local Similarity 62.7%; Pred. No. 2.4e-41;
Matches 94; Conservative 24; Mismatches 32; Indels 0; Gaps 0;

QY 16 ANSERTFIAIKPDGVORGLVGBIIKRFQKGRLVGLKFLQASEDLLKEHYTDLKDRPFF 75
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
Db 85 AEWERTFIAIKPDGVORGLISIIITFRKGYKLGIKVIVPSKDFQAQKHDLKERPFF 144
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
QY 76 TGLVKVMHSGPPVAMWVEGLNVVTKRVMLETNPADSKPGTIRGDFCIQVGRIIHGSD 135
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
Db 145 NGLCNFLSSGPVVAMWVEGEVIRYRKILIGATDPQKSEPTIRGDLAVTVGNRIIHGSD 204
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
QY 136 SVKSAREKTSIWLFPQEELVEYKSCAQNIY 165
| | | | | | | | | | | | | | | | | | | | : : : | | | | |
Db 205 GPETAKDEISLWFKPELVSYTSNAEKWIY 234
| | | | | | | | | | | | | | | | | | | | : : : | | | | |

RESULT 14
T14183
nucleoside-diphosphate kinase (EC 2.7.4.6) - common sunflower
C;Species: Helianthus annuus (common sunflower)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14183
R;Grayburn, W.S.; Vick, B.A.
submitted to the EMBL Data Library, September 1996

Query Match	58.2%;	Score 510;	DB 2;	Length 154;
Best Local Similarity	60.4%;	Pred. No. 2.7e-41;		
Matches 93;	Conservative 27;	Mismatches 32;	Indels 2;	Gaps 1;
Qy	15	MANSERFIAIKPDGVGRLNGEIIKEPQKGLVLGKFLQASED--LLKEHYHTLKDOR	72	
Db	1	MSNOEQFIIVKPDGVGRLVGNIIISFENRGFKLVAMKUTQPGQVHLEKHYEDUNT	60	
Qy	73	PFFTGVLKYMHSGPVAMVMEGLNVVKTGRVMLGETNPADSKPCTIRGDFCIVQGRNIIH	132	
Db	61	PFFAGLIKMYNSGPICAMVWEGDAVKTGRTILGATNPPLASAPCTIRGDFALDWMGRVCH	120	
Qy	133	GSDSVKSAEKESISLWFPQPEELVEYKSCAQNIYE	166	
Db	121	GSDSVENAKKEIALWFKPEELNOWNHHSAAWIPE	154	

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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:59 ; Search time 22.4654 Seconds
(without alignments)
650.999 Million cell updates/sec

Title: US-10-074-694-5
Perfect score: 803
Sequence: 1 MANLERTFAIKPDGVQVGL.....WFKPELVYKSCAHDWVE 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	803	100.0	152	2 A49798	nucleoside-diphosp
2	794	98.9	152	2 A38369	nucleoside-diphosp
3	793	98.8	152	2 S29241	nucleoside-diphosp
4	732	91.2	152	2 A45208	nucleoside-diphosp
5	729	90.8	166	2 A46557	nucleoside-diphosp
6	720	89.7	152	1 A33386	nucleoside-diphosp
7	620	77.2	153	2 S01908	nucleoside-diphosp
8	557.5	69.4	153	2 T21354	hypothetical prote
9	536.5	66.8	168	2 I39074	nucleoside-diphosp
10	534.5	66.6	153	2 JCA359	nucleoside-diphosp
11	525	65.4	154	2 T50459	nucleoside-diphosp
12	510.5	63.6	148	2 T14183	nucleoside-diphosp
13	509.5	63.4	149	2 S33170	nucleoside-diphosp
14	505	62.9	153	2 S37889	nucleoside-diphosp
15	505	62.9	237	2 T08909	hypothetical prote
16	504.5	62.8	148	2 S24165	nucleoside-diphosp
17	503	62.6	238	2 T01877	nucleoside-diphosp
18	500.5	62.3	149	2 S43330	nucleoside-diphosp
19	498	62.0	153	2 S60363	nucleoside-diphosp
20	495.5	61.7	149	2 T07042	nucleoside-diphosp
21	494.5	61.6	149	2 T17131	nucleoside-diphosp
22	487.5	60.7	147	2 S31444	nucleoside-diphosp
23	479	59.7	149	2 S76467	nucleoside-diphosp
24	468	58.3	151	1 T39099	nucleoside-diphosp
25	467.5	58.2	144	2 S47974	nucleoside-diphosp
26	465	57.9	151	2 G69345	nucleoside-diphosp
27	461	57.4	155	2 A49547	nucleoside-diphosp
28	460	57.3	220	2 B49547	nucleoside-diphosp
29	452	56.3	152	2 T51612	nucleoside-diphosp

ALIGNMENTS

RESULT 1

A49798
nucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H2 - human
N:Alternate names: c-myc transcription factor PuF; tumor metastasis inhibitor nm23-H2
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence revision 12-Mar-1999 #text_change 05-Oct-2004
C:Accession: A49798; B39838; I59581
R:Stahl, J.A.; Leone, A.; Rosengard, A.M.; Porter, L.; King, C.R.; Steeg, P.S.
Cancer Res. 51, 445-449, 1991
A:Title: Identification of a second human nm23 gene, nm23-H2.
A:Reference number: A49798; MUID:91105674; PMID:1988104
A:Accession: A49798
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-152 <STA>
A:Cross-references: UNIPROT:P22392; UNIPARC:UPI0000112864; GB:X58965; NID:g35069; PIDN:R:Gillies, A.M.; Presecan, E.; Vonica, A.; Lascu, I.
J. Biol. Chem. 266, 8784-8789, 1991
A:Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characterization
A:Reference number: A39838; MUID:91224972; PMID:1851158
A:Accession: B39838
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-152 <GIL>
A:Cross-references: UNIPARC:UPI0000112864
R:Postel, E.H.; Berberich, S.J.; Flint, S.J.; Ferrone, C.A.
Science 261, 478-480, 1993
A:Title: Human c-myc transcription factor PuF identified as nm23-H2 nucleoside diphosph
A:Reference number: I59581; MUID:93324921; PMID:8392752
A:Accession: I59581
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-152 <RES>
A:Cross-references: UNIPARC:UPI0000112864; GB:L16785; NID:g349475; PIDN:AAA60228.1; PID

30	452	56.3	231	2	T52586	nucleoside-diphosp
31	451	56.2	147	2	F83856	nucleoside diphosp
32	447	55.7	230	2	S52785	nucleoside-diphosp
33	445	55.4	149	2	D69666	nucleoside-diphosp
34	429	53.4	148	2	S31446	nucleoside-diphosp
35	428	53.3	233	2	S28226	nucleoside-diphosp
36	409	50.9	161	2	H84271	nucleoside diphosp
37	400	49.8	147	2	A11687	nucleoside diphosp
38	397	49.4	149	2	E89925	probable nucleosid
39	397	49.4	160	2	C71116	nucleoside diphosp
40	390	48.6	147	2	A11315	nucleoside diphosp
41	377	46.9	162	2	D75044	nucleoside-diphosp
42	375	46.7	140	2	H64457	nucleoside-diphosp
43	374	46.6	151	2	D69132	nucleoside-diphosp
44	357	44.5	191	2	F75266	nucleoside diphosp
45	355	44.2	138	2	D90164	hypothetical prote

Query Match 100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.8e-71;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFAIKPDGVQVGLVGEIIRFKFQKGRFLVAMKFLRASEHLKHQYIDLKDRPF 60
Db 1 MANLERTFAIKPDGVQVGLVGEIIRFKFQKGRFLVAMKFLRASEHLKHQYIDLKDRPF 60
QY 61 FFLGVKYNMSPVVMVWVGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

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|||||
Db      61  FPLGLVKYNSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
QY      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 2
A38369
nucleoside-diphosphate kinase (EC 2.7.4.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 05-Oct-2004
C:Accession: A41849; A38369; A42967
R:Heimerich, S.; Yarden, Y.; Pecht, I.
Biochemistry 31, 4574-4579, 1992
A:Title: A cromoglycate binding protein from rat mast cells of a leukemia line is a nucleoside-diphosphate kinase
A:Reference number: A41849; MUID:92256389; PMID:1316151
A:Accession: A41849
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-152 <HEM>
A:Cross-References: UNIPROT:P19804; UNIPARC:UPI000012FE93
R:Kimura, N.; Shimada, N.; Nomura, K.; Watanabe, K.
J. Biol. Chem. 265, 15744-15749, 1990
A:Title: Isolation and characterization of a cDNA clone encoding rat nucleoside diphosphate kinase
A:Reference number: A38369; MUID:90368787; PMID:2168422
A:Accession: A38369
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-152 <KIM>
A:Cross-References: UNIPARC:UPI000012FE93; GB:M55331; GB:J05588; NID:g205661; PIDN:AAA41
R:Ishikawa, N.; Shimada, N.; Munakata, Y.; Watanabe, K.; Kimura, N.
J. Biol. Chem. 267, 14366-14372, 1992
A:Title: Isolation and characterization of a gene encoding rat nucleoside diphosphate kinase
A:Reference number: A42967; MUID:9232552; PMID:1321145
A:Accession: A42967
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-152 <ISH>
A:Cross-References: UNIPARC:UPI000012FE93
A:Note: sequence extracted from NCBI backbone (NCBIN:108562, NCBI:P108564)
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:15-19/Region: ATP binding #status predicted
F:118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      98.9%; Score 794; DB 2; Length 152;
Best Local Similarity 98.0%; Pred. No. 1.4e-70;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  MANLERTFIAIKPDGVQVGLVGEIIRFPQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF 60
Db      1  MANLERTFIAIKPDGVQVGLVGEIIRFPQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF 60
QY      61  FPLGLVKYNSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
Db      61  FPLGLVKYNSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
QY      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 3
S29241
nucleoside-diphosphate kinase (EC 2.7.4.6) B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S29241
R:Urano, T.; Takamiya, K.; Furukawa, K.; Shiku, H.
FEBS Lett. 309, 358-362, 1992
A:Title: Molecular cloning and functional expression of the second mouse nm23/NDP kinase
```

```
A:Reference number: S29241; MUID:92387389; PMID:1325378
A:Accession: S29241
A:Molecule type: mRNA
A:Residues: 1-152 <URA>
A:Cross-References: UNIPROT:Q01768; UNIPARC:UPI0000038FD; EMBL:X68193; NID:g53353; PIDN:
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:15-19/Region: ATP binding #status predicted
F:118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      98.8%; Score 793; DB 2; Length 152;
Best Local Similarity 98.0%; Pred. No. 1.8e-70;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  MANLERTFIAIKPDGVQVGLVGEIIRFPQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF 60
Db      1  MANLERTFIAIKPDGVQVGLVGEIIRFPQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF 60
QY      61  FPLGLVKYNSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
Db      61  FPLGLVKYNSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
QY      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 4
A45208
nucleoside-diphosphate kinase (EC 2.7.4.6) isoform beta - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C:Accession: A45208
R:Shimada, N.; Ishikawa, N.; Munakata, Y.; Toda, T.; Watanabe, K.; Kimura, N.
J. Biol. Chem. 268, 2583-2589, 1993
A:Title: A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolat:
A:Reference number: A45208; MUID:93155067; PMID:8381409
A:Accession: A45208
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-152 <SHI>
A:Cross-References: UNIPROT:Q05982; UNIPARC:UPI000012FE91; GB:D13374; NID:g286231; PIDN:
A:Experimental source: skeletal muscle
A:Note: sequence extracted from NCBI backbone (NCBI:P124170)
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:15-19/Region: ATP binding #status predicted
F:118/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      91.2%; Score 732; DB 2; Length 152;
Best Local Similarity 90.1%; Pred. No. 1.7e-64;
Matches 137; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY      1  MANLERTFIAIKPDGVQVGLVGEIIRFPQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF 60
Db      1  MANSERTFIAIKPDGVQVGLVGEIIRFPQKGFRLVGLKFIQASEDLLEHVIDLKDRPF 60
QY      61  FPLGLVKYNSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
Db      61  FSLGLVKYMHSGPPVAMVWVWVGLNVVKTGRVLMGETNPADSKPCTIRGDFCIQVGRNIIHGS 120
QY      121  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db      121  DSVKSAEKEISLWFKPEELVDYKSCAQNWIYE 152

RESULT 5
A46557
nucleoside-diphosphate kinase (EC 2.7.4.6) - mouse (fragment)
N:Alternate names: differentiation-inhibiting factor; tumor metastasis inhibitor NM23
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 05-Oct-2004
C:Accession: A46557; B33386; I52807; JN0281
```

R;Steeg, P.S.; Bevilacqua, G.; Kopper, L.; Thorgeirsson, U.P.; Talmadge, J.E.; Liotta, L. J. Natl. Cancer Inst. 80, 200-204, 1988
A>Title: Evidence for a novel gene associated with low tumor metastatic potential.
A/Reference number: A46557; MUID:80155671; PMID:3346912
A/Accession: A46557
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-166 <ROS>
A/Cross-references: UNIPROT:P15532; UNIPARC:UPI000016CF64; GB:M35970; NID:g200066; PIDN: A/Note: the authors translated the codon TGG for residue 163 as Tyr
R;Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M. Nature 342, 177-180, 1989
A>Title: Reduced Nm23/awd protein in tumour metastasis and aberrant Drosophila development
A/Reference number: A33386; MUID:90044071; PMID:2509941
A/Accession: B33386
A>Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 15-166 <ROS>
A/Cross-references: UNIPARC:UPI000000188F
R;Leone, A.; Flatow, U.; King, C.R.; Sandeen, M.A.; Margulies, I.M.; Liotta, L.A.; Steeg Cell 65, 25-35, 1991
A>Title: Reduced tumor incidence, metastatic potential, and cytokine responsiveness of h
A/Reference number: I52807; MUID:91191558; PMID:2013093
A/Accession: I52807
A>Status: preliminary; translated from GB/EMBL/DBBJ
A/Molecule type: mRNA
A/Residues: 15-166 <RES>
A/Cross-references: UNIPARC:UPI000000198F; GB:M65037; NID:g200068; PIDN:AAA63391.1; PID: R;Okabe-Kado, J.; Kasukabe, T.; Honma, M.; Hayashi, W.J.; Hozumi, M. Biochem. Biophys. Res. Commun. 182, 987-994, 1992
A>Title: Identity of a differentiation inhibiting factor for mouse myeloid leukemia cell
A/Reference number: JN0281; MUID:92171977; PMID:1311576
A/Accession: JN0281
A/Molecule type: protein
A/Residues: 19-21;23-25; 'M';54-55; 'R';57-59; 'E';61,63; 'Q'; 'YI';78-98;100-103;105-113;115
A/Cross-references: UNIPARC:UPI0000055EF8; UNIPARC:UPI000015759C; UNIPARC:UPI0000175709; 70E; UNIPARC:UPI000017570F; UNIPARC:UPI0000175710
A/Experimental source: myeloid leukemia cell
C/Comment: This factor is Nm23/nucleoside diphosphate kinase (EC 2.7.4.6) involved in tu
C/Genetics:
A/Gene: nm23
A/Superfamily: nucleoside diphosphate kinase
C/Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;29-33/Region: ATP binding #status predicted
F;132/Active site: His (phosphohistidine intermediate) #status predicted
Query Match 90.8%; Score 729; DB 2; Length 166;
Best Local Similarity 90.1%; Pred. No. 3.7e-64;
Matches 137; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 1 MANLERTFAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 15 MANSERTFAIKPDGVQVGLVGEIIRFEQKGFRLVGLKFLQASEDLKHEHYIDLKDRPF 74
QY 61 FPLGLVKYMGSGPVVAMVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 75 FTGLVKYMGSGPVVAMVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYE 152
DB 135 DSVKSAEKEISLWFKPEELVDYKSCAQNWIYE 166
RESULT 6
A33386
nucleoside-diphosphate kinase (EC 2.7.4.6) nm23-Hig - human
N/Alternate names: nm23-Hig protein; probable metastatic suppressor nm23-H1
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text change 05-Oct-2004
A/Accession: A33386; S45376; A39831; A56882; B43931
R;Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M. Nature 342, 177-180, 1989
A>Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila developme

A/Reference number: A33386; MUID:90044071; PMID:2509941
A/Accession: A33386
A>Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-152 <ROS>
A/Cross-references: UNIPROT:P15531; UNIPARC:UPI0000112099; GB:X75598; NID:g468541; PIDN: R;Dooley, S.; Seib, T.; Engel, M.; Theisinger, B.; Janz, H.; Piontek, K.; Zhang, K.D.; We Hum. Genet. 93, 63-66, 1994
A>Title: Isolation and characterization of the human genomic locus coding for the putati
A/Reference number: S45376; MUID:94095204; PMID:8270257
A/Accession: S45376
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-152 <DOO>
A/Cross-references: UNIPARC:UPI0000112099; EMBL:X75598; NID:g468541; PIDN:CAAS3270.1; P R;Gilles, A.M.; Presecan, E.; Vonica, A.; Lascau, I. J. Biol. Chem. 266, 8784-8789, 1991
A>Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characterizat
A/Reference number: A39838; MUID:91224972; PMID:1851158
A/Accession: A39838
A/Molecule type: protein
A/Residues: 1-152 <GIL>
A/Cross-references: UNIPARC:UPI0000112099
R;Haliat, N.; Reim, D.R.; Melhem, R.F.; Zhu, X.X.; Eckerskorn, C.; Brodeur, G.M.; Reynol J. Clin. Invest. 88, 341-345, 1991
A>Title: High levels of p19/nm23 protein in neuroblastoma are associated with advanced t
A/Reference number: A43931; MUID:91277302; PMID:2056128
A/Accession: A43931
A/Molecule type: protein
A/Residues: 7-18;40-49;89-94 <HAI>
A/Cross-references: UNIPARC:UPI000004BCA0; UNIPARC:UPI00001726A4; UNIPARC:UPI00001726A5
A/Note: sequence modified after extraction from NCBI backbone
R;Wang, L.; Patel, U.; Ghosh, L.; Chen, H.C.; Banerjee, S. Cancer Res. 53, 717-720, 1993
A>Title: Mutation in the nm23 gene is associated with metastasis in colorectal cancer.
A/Reference number: A56882; MUID:93153759; PMID:7916650
A/Accession: A56882
A/Molecule type: mRNA
A/Residues: 1-86; 'SAYKLAGTLYMAVILWVRRRSACGFTLRNW' <WAN>
A/Cross-references: UNIPARC:UPI00001726A6
A/Note: mutant sequence shown (tumor 10) was extracted from NCBI backbone; wild type se
A/Note: sequence extracted from NCBI backbone (NCBI:124581, NCBI:124584)
C/Genetics:
A/Gene: GDB:NME1; nm23-H1
A/Cross-references: GDB:127965; OMIM:156490
A/Map position: 17q21-17q22
A/Introns: 43/1; 77/2; 114/2
C/Superfamily: nucleoside diphosphate kinase
C/Keywords: ATP binding; blocked amino end; hexamer; phosphohistidine; phosphoprotein; i
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
Query Match 89.7%; Score 720; DB 1; Length 152;
Best Local Similarity 88.2%; Pred. No. 2.5e-63;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 MANLERTFAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MANSERTFAIKPDGVQVGLVGEIIRFEQKGFRLVGLKFLQASEDLKHEHYIDLKDRPF 60
QY 61 FPLGLVKYMGSGPVVAMVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FAGLVKYMHSFPVAMVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYE 152
DB 121 DSVSAEKEISLWFKPEELVDYKSCAQNWIYE 152
RESULT 7
S01908
nucleoside-diphosphate kinase (EC 2.7.4.6) - fruit fly (Drosophila melanogaster)
N/Alternate names: K-pn protein; killer-of-prune protein

C:Species: Drosophila melanogaster
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S01908
R:Bl998, J.; Tripoulas, N.; Hersperger, E.; Dearolf, C.; Shearn, A.
Genes Dev. 2, 1333-1343, 1988
A:Title: Analysis of the lethal interaction between the prune and killer of prune mutants
A:Reference number: S01908; MUID:89079007; PMID:2849580
A:Accession: S01908
A:Molecule type: mRNA
A:Residues: 1-153 <BIG>
A:Cross-references: UNIPROT:P08879; UNIPARC:UPI00000011C4; EMBL:X13107; NID:g7634; PIDN:
C:Genetics:
A:Gene: awd
A:Map position: 3 100C-D
A:Cross-references: FlyBase:FBgn0000150
A:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:16-20/Region: ATP binding #status predicted
F:119/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 77.2%; Score 620; DB 2; Length 153;
Best Local Similarity 77.5%; Pred. No. 1.6e-53;
Matches 117; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 2 ANLERTFAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPFF 61
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 3 ANKERTFINVKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPFF 62
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

QY 62 PGLVKNMNSGPPVAMVWEGNLVTKTRVMLGNTNPDSPKGTIRGDFCIQVGRNIIHGS 121
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 63 PGLVKNMNSGPPVAMVWEGNLVTKTRVMLGNTNPDSPKGTIRGDFCIQVGRNIIHGS 122
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

QY 122 SVKSAEKEISLWFKPEELVDYKSCAHDWVE 152
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 123 AVESAEEKIALWFNEKELVTWTPAAKDWIYE 153
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

RESULT 8
T21354
hypothetical protein F25H2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21354
R:Wilkinson, J.
Submitted to the EMBL Data Library, September 1996
A:Reference number: Z19411
A:Accession: T21354
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-153 <WIL>
A:Cross-references: UNIPROT:Q93576; UNIPARC:UPI000007F609; EMBL:Z79754; PIDN:CAB02101.1;
A:Experimental source: clone F25H2
C:Genetics:
A:Gene: CESP:F25H2.5
A:Map position: 1
A:Introns: 18/2; 49/3
C:Superfamily: nucleoside diphosphate kinase

Query Match 69.4%; Score 557.5; DB 2; Length 153;
Best Local Similarity 68.6%; Pred. No. 2.2e-47;
Matches 105; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 1 MANLERTFAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPFF 60
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 1 MSNTERTFIAIKPDGVHRLGVLGKIIARPEERGGYKLVAKQMTASKAHLEVHYQDLKDRPFF 60
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

QY 61 PGLVKNMNSGPPVAMVWEGNLVTKTRVMLGNTNPDSPKGTIRGDFCIQVGRNIIHGS 120
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 61 PFLSLEYMNSGPPVAMVWGLDVVQGRSLMGLATNPLASAPGTIRGDFCIQVGRNIIHGS 120
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

QY 121 DSVKSAEKEISLWFKPEELVDYKS-CAHDWVE 152
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 121 DAVDSANREIAHWFKEEINDVSPFINSWVE 153
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

RESULT 9

I39074

nucleoside-diphosphate kinase (BC 2.7.4.6) DR-nm23 - human
N:Alternate names: DR-nm23 protein; non-metastatic cell-expressed protein 3
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I39074
R:Venturelli, D.D.; Martinez, R.R.; Calabretta, B.B.
Proc. Natl. Acad. Sci. U.S.A. 92, 7435-7439, 1995
A:Title: Overexpression of DR-nm23, a protein encoded by a member of the nm23 gene family
A:Reference number: I39074; MUID:95365382; PMID:7638209
A:Accession: I39074
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-168 <RES>
A:Cross-references: UNIPROT:Q13232; UNIPARC:UPI0000149FCF; EMBL:U29656; NID:g1051255; PI:
C:Genetics:
A:Gene: GDB:NME3; DR-nm23
A:Cross-references: GDB:5215169; OMIM:601817
A:Map position: 16q13-16q13
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:32-36/Region: ATP binding #status predicted
F:134/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 66.8%; Score 536.5; DB 2; Length 168;
Best Local Similarity 64.9%; Pred. No. 2.9e-45;
Matches 96; Conservative 33; Mismatches 18; Indels 1; Gaps 1;

QY 5 ERTTAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPFFPGL 64

DDB 22 ERTFLAVKPDGVQVRLVGEIVRRFERKGLVALLVQSSSELLREHFAELRERPFYGR 81

QY 65 VKYMNNSGPPVAMVWEGNLVTKTRVMLGNTNPDSPKGTIRGDFCIQVGRNIIHGS 124
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 82 VKYMASGPPVAMVWGLDVVTSRALIGATNPADAPGTIRGDFCIQVGRNIIHGS 140
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

QY 125 SAEKEISLWFKPEELVDYKSCAHDWVE 152
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |
DDB 141 SARREIALWFRADLELLCWEDSAGHWLYE 168
| | | | | - - - - - | | | | | - - - - - | | | | | - - - - - | | | | |

RESULT 10

JC4359

nucleoside-diphosphate kinase (BC 2.7.4.6) - nematode (Brugia malayi)
C:Species: Brugia malayi
C:Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4359
R:Chosh, I.; Raghavan, N.; FitzGerald, P.C.; Scott, A.L.
Gene 164, 261-266, 1995
A:Title: Nucleoside diphosphate kinase from the parasitic nematode Brugia malayi.
A:Reference number: JC4359; MUID:96069592; PMID:7590340
A:Accession: JC4359
A:Molecule type: mRNA
A:Residues: 1-153 <GHO>
A:Cross-references: UNIPROT:P48817; UNIPARC:UPI000012FB9C; GB:U18906; NID:g619942; PIDN:
C:Comment: This enzyme is a pivotal enzyme in the synthesis of nucleotide triphosphates
de triphosphates, supplying GTP for GTP-binding proteins and a role in signal transduction
C:Genetics:
A:Gene: ndk
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:13-17/Region: ATP binding #status predicted
F:106/Active site: Arg #status predicted
F:119/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 66.6%; Score 534.5; DB 2; Length 153;
Best Local Similarity 65.4%; Pred. No. 4e-45;
Matches 100; Conservative 24; Mismatches 28; Indels 1; Gaps 1;

QY 1 MANL-ERTFIAIKPDGVQVGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRP 59


```
Db 1 MSNKTERTICIKPDVAVQRLGKIFERPEQRGYKLVAMKMLKATKSHLEIHYBLOQKP 60
QY 60 PFPGLVKYNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIH 119
Db 61 FFDNLGVYNSGPFVAVMWEGVJVVVKQARQMLGATNPLNSMPTGIRGDFSIQTRNIVHG 120
QY 120 SDSVKSAAKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 SDSLPSAEREITHWFKPEELCEWSSATATWVYE 153

RESULT 11
T50459
nucleoside-diphosphate kinase (EC 2.7.4.6) [validated] - Neurospora crassa
N:Contains: protein kinase
C:Species: Neurospora crassa
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: T50459
R:Ogura, Y.; Yoshida, Y.; Ichimura, K.; Aoyagi, C.; Yabe, N.; Hasunuma, K.
Eur. J. Biochem. 266, 709-714, 1999
A:Title: Isolation and characterization of Neurospora crassa nucleoside-diphosphate kinase
A:Reference number: Z25071; MUID:20050582; PMID:10583364
A:Accession: T50459
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-154 <OGU>
A:Cross-references: UNIPROT:Q9UUY8; UNIPARC:UPI000012FE98; EMBL:D88148; NID:g5771347; PI
C:Genetics:
A:Intons: 7/2; 112/3
A:Note: ndk-1
C:Function: <NDK1>
A:Description: EC 2.7.4.6 [validated, MUID:20050582]; phosphorylates nucleoside diphosph
C:Function: <PKIN>
A:Description: phosphorylates proteins in vitro [validated, MUID:20050582]
A:Note: acts as a signal transducer by phosphorylating proteins
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: phosphoprotein; phosphotransferase

Query Match 65.4%; Score 525; DB 2; Length 154;
Best Local Similarity 62.3%; Pred. No. 3.4e-44;
Matches 96; Conservative 25; Mismatches 31; Indels 2; Gaps 1;

QY 1 MANLRTFAIKPDGVQVGLVGBIIKRFQKGRFLVAMKFLRASEH--LKQHYIDLKDR 58
Db 1 MSNQEFTFAVRKPDGVQVGLVGNIIISRFENRGFKLVAMKLTQPGQVHLEKHEDLNTK 60

QY 59 PFPGLVKYNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIH 118
Db 61 PFPAGLIKYNISGPICAMVWEGKDAVKTGRTILGATNPLASAPGTIRGDFALDMGRNVCH 120

QY 119 GSDSVKSAAKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 GSDSVENAKKETALWFKPEELQNMNHHSAAWIFE 154

RESULT 12
T14183
nucleoside-diphosphate kinase (EC 2.7.4.6) - common sunflower
C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14183
R:Grayburn, W.S.; Vick, B.A.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z17907
A:Accession: T14183
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-148 <GRA>
A:Cross-references: UNIPROT:Q96559; UNIPARC:UPI000012FEAB; EMBL:U72142; NID:g16119957; PI
C:Function:
A:Description: catalyzes transfer of the gamma-phosphate group from ATP to nucleoside di
cid synthesis, UTP for polysaccharide synthesis, CTP for lipid synthesis and GTP for prd
```

```
by modulating GTP levels
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; phosphohistidine; phosphoprotein; phosphotransferase; pyrimidi

Query Match 63.6%; Score 510.5; DB 2; Length 148;
Best Local Similarity 63.8%; Pred. No. 8.7e-43;
Matches 95; Conservative 22; Mismatches 31; Indels 1; Gaps 1;

QY 4 LERTFIAIKPDGVQVGLVGEIIRKFEQGRFLVAMKFLRASEHHLKQHYIDLKDRPFPGL 63
Db 1 MEQTFIMIKPDGVQVGLVGEIIRFEKKGFTLKGLKLLTVDAQFAEKHYADLSAKPFFNG 60

QY 64 LVKYNNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHSDSV 123
Db 61 LVEYIISGPVAVMWEGKVNVTGRTKIIGATNPAESPFGTIRGDFPAIDIGRNVIHGSDAV 120

QY 124 KSAKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 ESAKKEIGLMP-PEGVANWSSSLHPWIYE 148

RESULT 13
S33170
nucleoside-diphosphate kinase (EC 2.7.4.6) - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S46513; S33170
R:Finan, P.M.; White, I.R.; Redpath, J.B.C.; Millner, P.A.
Plant Mol. Biol. 25, 59-67, 1994
A:Title: Molecular cloning, sequence determination and heterologous expression of nucle
A:Reference number: S46513; MUID:94272014; PMID:8003697
A:Accession: S46513
A:Molecule type: mRNA
A:Residues: 1-149 <PI2>
A:Cross-references: UNIPROT:P47922; UNIPARC:UPI000012FE7F; EMBL:X71388; NID:g296173; PI
A:Note: submitted to the EMBL Data Library, April 1993
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F:13-17/Region: ATP binding #status predicted
F:116/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 63.4%; Score 509.5; DB 2; Length 149;
Best Local Similarity 63.5%; Pred. No. 1.1e-42;
Matches 94; Conservative 21; Mismatches 32; Indels 1; Gaps 1;

QY 5 BRTETAIKPDGVQVGLVGEIIRKFEQGRFLVAMKFLRASEHHLKQHYIDLKDRPFPGL 64
Db 3 EOTFIMIKPDGVQVGLVGEIIRFEKKGFTLKGLFVNVERAFAEKHYADLSAKPFFSGL 62

QY 65 VKYNNNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHSDSV 124
Db 63 VDYIISGPVAVMWEGKVNVTGRTKIIGATNPAQSEPGTIRGDFPAIDIGRNVIHGSDAVE 122

QY 125 SAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 123 SANKETALWF-PEGAANWESSLSHWIYE 149

RESULT 14
S37889
nucleoside-diphosphate kinase (EC 2.7.4.6) [validated] - yeast (Saccharomyces cerevisia
N:Alternate names: protein YKL067w; protein YKL333
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: S37889; S44519; JN0754; S39174
R:Rasmussen, S.; von Wettstein, D.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37872
A:Accession: S37889
A:Molecule type: DNA
A:Residues: 1-153 <RAS>
A:Cross-references: UNIPROT:P36010; UNIPARC:UPI0000037234; EMBL:Z28067; NID:g486092; PI
A:Experimental source: strain S288C
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:59 ; Search time 126.667 Seconds
(without alignments)
527.255 Million cell updates/sec

Title: US-10-074-694-5

Perfect score: 803

Sequence: 1 MANLERTFIAIKPDGVORGL.....WFKPEELVDYKSCAHDWVE 152

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	803	100.0	152	2	Aay07000 mm23-H2 p
2	803	100.0	152	4	Aag80282 Human NM2
3	803	100.0	152	5	Aag79337 Mature hu
4	803	100.0	152	6	Abu89707 Protein d
5	803	100.0	152	8	Adh17091 Human nm2
6	803	100.0	152	8	Abm81902 Tumour-as
7	803	100.0	152	8	Adp23162 PRO polyp
8	803	100.0	152	9	Adx05640 Cyclin-de
9	803	100.0	152	9	Ady14458 PRO polyp
10	803	100.0	152	9	Ady19693 PRO polyp
11	803	100.0	167	9	Aea89623 Tumor met
12	803	100.0	176	3	Aab14812 Human nm2
13	803	100.0	176	5	Aao26423 Protein o
14	803	100.0	176	5	Aag79336 Human NM2
15	798	99.4	151	9	Aea90109 Human nuc
16	794	98.9	190	5	Abp51330 Human MDD
17	793	98.8	152	4	Aag80283 Murine NM
18	788	98.1	149	8	Adr66920 Human pro
19	788	98.1	149	8	Adr66022 Human pro
20	749	93.3	155	8	Abos8327 Human gen
21	733	91.3	152	4	Aab60681 Bovine nu
22	732	91.2	152	4	Aab60680 Bovine nu
23	729	90.8	152	4	Aag80281 Murine NM
24	723	90.0	223	4	Aam78984 Human pro

RESULT 1
AAY07000
ID AAY07000 standard; protein; 152 AA.
XX AC AAY07000;
XX DT 02-JUL-1999 (first entry)
XX DE mm23-H2 protein sequence.
XX KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
XX OS Homo sapiens.
XX FN WO9904265-A2.
XX PD 28-JAN-1999.
XX PF 15-JUL-1998; 98WO-US014679.
XX PR 17-JUL-1997; 97US-00896164.
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX (LUDW-) LUDWIG INST CANCER RES.
PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
PI O'hare M, Obata Y, Pfeundschtuh M, Tureci O, Sahin U;
XX WPI; 1999-132448/11.
XX N-PSDB; AAX40201.
PT New isolated cancer associated nucleic acids and polypeptides - isolated
PT using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.
XX Example 8; Page 787; 787pp; English.
XX The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically

ALIGNMENTS

CC The sequences given in AAG79335-38 show the related human proteins NM23-H1 and H2s. These proteins are products of different genes, with NM23-H1 being localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for selection of treatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alteration in its regulation may be an early stage in the metastatic cascade.

CC Allelic or homozygous deletion of the gene is detected in some primary tumour cells

XX

SQ

Sequence 152 AA;

Query Match 100.0%; Score 803; DB 5; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGVNLVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGVNLVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIHGS 120

Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 4

ABU89707
ID ABU89707 standard; protein; 152 AA.

AC ABU89707;

DT 10-JUL-2003 (first entry)

DE Protein differentially expressed in cardiovascular disease #1.

XX Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
KW myocardial infarction; cardiast; antiarteriosclerotic; antianginal;
KW gene therapy; differential gene expression.

XX Homo sapiens.

XX WO2003031650-A2.

XX 17-APR-2003.

PF 02-OCT-2002; 2002WO-EP011034.

XX 08-OCT-2001; 2001GB-00024145.

PA (FARB) BAYER AG.

PI Munnes M, Gehrman M, Wick M, Schmitz G;

XX WPI; 2003-403108/38.

DR N-PSDB; ACA89880.

XX Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
PT of a polynucleotide in a biological sample comprises detecting a
PT hybridization complex.

PS Claim 3; Page 251-252; 454pp; English.

XX The invention describes a method of predicting, diagnosing or prognosing
CC a cardiovascular disease by detection of a polynucleotide in a biological
CC sample comprises hybridising at least one of the polynucleotide to a
CC nucleic acid material of a biological sample, thus forming a
CC hybridisation complex, and detecting the hybridisation complex. The

CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
CC are useful for preparing compositions for preventing, predicting or
CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
CC This sequence represents a protein identified in the invention a being
CC differentially expressed in individuals with cardiovascular disease

XX

SQ

Sequence 152 AA;

Query Match 100.0%; Score 803; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60

Qy 61 FPGLVKYMNSGPPVAMVWEGVNLVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGVNLVKTGRVLMGETNPADSKPTGTIRGDFCIVQGRNIHGS 120

Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 5

ADH17091
ID ADH17091 standard; protein; 152 AA.

AC ADH17091;

DT 11-MAR-2004 (first entry)

DE Human nm23-H2 gene protein.

XX tyrosine kinase activity; type 1 plasminogen activator inhibitor; PAI-1;
KW TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin;
KW vascular endothelial growth factor; VEGF; placental growth factor; PLGF;
KW migration inhibitory factor; MIG; human; nm23-H2.

XX Homo sapiens.

XX WO2003097854-A2.

XX 27-NOV-2003.

XX 19-MAY-2003; 2003WO-US015711.

XX 17-MAY-2002; 2002US-0380872P.

PR 24-FEB-2003; 2003US-0448874P.

PR 24-FEB-2003; 2003US-0448922P.

XX (SUGE-) SUGEN INC.

XX Morimoto A, Deprimo S, O'farrell A, Smolich BD, Manning WC;

PI Walter SA, Schilling JW, Cherrington J;

XX WPI; 2004-042604/04.

DR N-PSDB; ADH17090.

XX Determining whether a test compound inhibits tyrosine kinase activity in
PT a mammal by exposing the mammal to the test compound and measuring in the
PT mammal the level of at least one of the measured proteins or mRNA
PT transcripts.

PS Disclosure; SEQ ID NO 90; 408pp; English.

XX The invention relates to a novel method for determining whether a test
CC compound inhibits tyrosine kinase activity in a mammal comprising
CC measuring in the mammal the level of at least one of the proteins and/or
CC mRNA transcripts or genes for such proteins comprising type 1 plasminogen
CC activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of

CC metalloproteinase 1), vinculin, vascular endothelial growth factor
CC (VEGF), placental growth factor (PLGF), VEGF/PLGF heterodimers or
CC migration inhibitory factor (MIG), exposing the mammal to the test
CC compound and then measuring in the mammal the level of at least one of
CC the proteins and/or mRNA transcripts previously measured. The method of
CC the invention may be useful for determining whether a test compound
CC inhibits tyrosine kinase activity in a mammal. The current sequence is
CC that of the tyrosine kinase activity inhibition-related protein of the
CC invention.

XX
SQ Sequence 152 AA;

Query Match 100.0%; Score 803; DB 8; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60

QY 61 FPGLVKYMNSGPVVMVWEGNLVVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FPGLVKYMNSGPVVMVWEGNLVVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVE 152

RESULT 6
ABM81902 ID ABM81902 standard; protein; 152 AA.
XX AC ABM81902;
XX DT 18-NOV-2004 (first entry)
XX DE Tumour-associated antigenic target (TAT) polypeptide PRO3637, SEQ:4888.
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX tumour; diagnosis; cell proliferative disorder; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX central nervous system cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; melanoma; leukaemia; hybridisation probe;
XX chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN W02004030615-A2.
XX PD 15-APR-2004.
XX PF 29-SEP-2003; 2003WO-US028547.
XX PR 02-OCT-2002; 2002US-0414971P.
XX PA (GETH) GENENTECH INC.
XX PI Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX DR N-PSDB; ACN40229.
XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.

XX Claim 12; SEQ ID NO 4888; 7273pp; English.
XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are

CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

XX
SQ Sequence 152 AA;

Query Match 100.0%; Score 803; DB 8; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60

QY 61 FPGLVKYMNSGPVVMVWEGNLVVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FPGLVKYMNSGPVVMVWEGNLVVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVE 152

RESULT 7
ADP23162 ID ADP23162 standard; protein; 152 AA.
XX AC ADP23162;
XX DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:256.
XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN W02004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH) GENENTECH INC.
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;
XX Wu TD;
XX WPI; 2004-419628/39.
XX DR N-PSDB; ADP23161.
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX renal disease, or demyelinating diseases of the central or peripheral

PT nervous system.
PS Claim 7; SEQ ID NO 256; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplant associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
XX of the invention.
XX
SQ Sequence 152 AA;

Query Match 100.0%; Score 803; DB 8; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVQGLVGEIIRKPEQGFRLVAMKFLRASEEHLKQHYIDLKORPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRKPEQGFRLVAMKFLRASEEHLKQHYIDLKORPF 60
QY 61 FPGVLKYMNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
DB 61 FPGVLKYMNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 8
ADX05640
ID ADX05640 standard; protein; 152 AA.
AC ADX05640;
XX
XX 21-APR-2005 (first entry)
XX
XX Cyclin-dependent kinase modulation biomarker SEQ ID NO 205.
DE
XX
XX cytostatic; cyclin-dependent kinase; cdk; biomarker.
KW
XX
XX Homo sapiens.
OS
XX
XX WO2005012875-A2.
FN
XX
XX 10-FEB-2005.
PD
XX
XX 29-JUL-2004; 2004WO-US024424.
PF
XX
XX 29-JUL-2003; 2003US-0490890P.
PR
XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
XX WPI; 2005-163068/17.
DR N-PSDB; ADX05639.
XX
XX Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
XX Claim 5; SEQ ID NO 205; 141pp; English.
XX
XX This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence represents a biomarker used in the method of the invention.
XX
XX Sequence 152 AA;

Query Match 100.0%; Score 803; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVQGLVGEIIRKPEQGFRLVAMKFLRASEEHLKQHYIDLKORPF 60
DB 1 MANLERTFIAIKPDGVQGLVGEIIRKPEQGFRLVAMKFLRASEEHLKQHYIDLKORPF 60
QY 61 FPGVLKYMNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
DB 61 FPGVLKYMNSGPVAVMWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

RESULT 9
ADY14458
ID ADY14458 standard; protein; 152 AA.
XX
XX ADY14458;
AC
XX
XX 05-MAY-2005 (first entry)
XX
XX PRO polypeptide SEQ ID NO 264.
DE
XX
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Antiallergic; ds; gene; diagnosis.
OS
XX
XX Homo sapiens.
XX
XX WO2005016962-A2.
FN
XX
XX 24-FEB-2005.
PD

XX PF 11-AUG-2004; 2004WO-US026249.
XX PF 11-AUG-2003; 2003US-0493546P.
XX PA (GETH) GENENTECH INC.
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX DR WPI; 2005-182330/19.
XX PF New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX PS Claim 8; SEQ ID NO 264; 158pp; English.
XX CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC competition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX SQ Sequence 152 AA;
Query Match 100.0%; Score 803; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
QY 61 FPGLVKYMNSGPVVMWVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FPGLVKYMNSGPVVMWVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKESLWFKPEELVDYKSCAHDWYVE 152
DB 121 DSVKSAEKESLWFKPEELVDYKSCAHDWYVE 152
RESULT 10
ADY19693
ID ADY19693 standard; protein; 152 AA.
XX AC ADY19693;
XX DT 05-MAY-2005 (first entry)
XX DE PRO polypeptide SEQ ID NO 5499.
XX KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; diagnosis.
XX OS Homo sapiens.
XX PN WO2005016962-A2.
XX PD 24-FEB-2005.
XX PF 11-AUG-2004; 2004WO-US026249.
XX PR 11-AUG-2003; 2003US-0493546P.
XX PA (GETH) GENENTECH INC.
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX

DR WPI; 2005-182330/19.
XX PF New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX PS Claim 8; SEQ ID NO 5499; 158pp; English.
XX CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.
XX SQ Sequence 152 AA;
Query Match 100.0%; Score 803; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MANLERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
QY 61 FPGLVKYMNSGPVVMWVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FPGLVKYMNSGPVVMWVMEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKESLWFKPEELVDYKSCAHDWYVE 152
DB 121 DSVKSAEKESLWFKPEELVDYKSCAHDWYVE 152
RESULT 11
AEA89623
ID AEA89623 standard; protein; 167 AA.
XX AC AEA89623;
XX DT 25-AUG-2005 (first entry)
XX DE Tumor metastases treatment-related human PRUNE protein SeqId11.
XX KW metastasis; therapeutic; gene expression; cytostatic; tumor;
KW breast tumor; sarcoma; nervous system tumor; prostate tumor;
KW pancreas tumor; colon tumor; rectal tumor; medulloblastoma;
KW b-cell lymphoma; t-cell lymphoma; multiple myeloma; lung tumor; cancer.
XX OS Homo sapiens.
XX PN WO2005056043-A2.
XX PD 23-JUN-2005.
XX PF 10-DEC-2004; 2004WO-IT000689.
XX PR 11-DEC-2003; 2003IT-RM000572.
XX PA (ZOLL/) ZOLLO M.
XX PI Zoilo M;
XX DR WPI; 2005-445065/45.
XX PF Use of inhibitors of human-PRUNE cyclic nucleotide phosphodiesterase for
PT preparation of medicament in the treatment of tumor metastases associated
PT with overexpression of human-PRUNE.
XX PS Example 4; SEQ ID NO 11; 89pp; English.
XX CC This invention relates to a novel method for preparing a medicament for
CC the treatment of tumor metastases associated with overexpression of human
CC -PRUNE. The method comprise using inhibitors of human-PRUNE cyclic

CC abnormalities of DNAs in normal or cancer cells to aid in predicting the
CC genetic predisposition for developing cancer. The human nm23 protein can
CC be employed to produce nm23 antibodies. This sequence represents the nm23
CC -H2S protein of the invention

XX SQ Sequence 176 AA;
Query Match 100.0%; Score 803; DB 5; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.6e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 25 MANLERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 84
QY 61 FPGLVKYMNSGPPVAMVWVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 85 FPGLVKYMNSGPPVAMVWVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 144
QY 121 DSVKSAEKETSLWFKPEELVDYKSCAHDWVYE 152
Db 145 DSVKSAEKETSLWFKPEELVDYKSCAHDWVYE 176

RESULT 14
AEA90109
ID AAG79336 standard; protein; 176 AA.
XX AC AAG79336;
XX DT 21-AUG-2002 (first entry)
XX DE Human NM23-H2S encoded from full length cDNA.
XX KW NM23-H1; NM23-H2S; aggressiveness; metastatic potential; tumour;
KW cancer susceptibility; early-onset familial breast cancer.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Protein 25..176
FT /label= Mature NM23-H2S
XX US6329198-B1.
XX PD 11-DEC-2001.
XX PF 18-JUN-1999; 99US-00335948.
XX PR 18-OCT-1989; 89US-00422801.
XX PR 11-DEC-1991; 91US-00806932.
XX PR 07-JUN-1995; 95US-00475684.
XX (USHE-) US DEPT SEC HEALTH & HUMAN SERVICES.
XX PA King CR, Steeg PS, Liotta LA;
XX WPI; 2002-121137/16.
XX N-PSDB; AA172992.
XX New human NM23 protein, useful for diagnosis and prognosis of cancer, and
XX assessment of aggressiveness and susceptibility.
XX Claim 3; Col 19-22; 23pp; English.
XX The sequences given in AAG79335-38 show the related human proteins NM23-
XX H1 and H2S. These proteins are products of different genes, with NM23-H1
XX being localized to chromosome 17. These proteins are used to predict
XX aggressiveness (metastatic potential) of human tumours and in genetic
XX tests for cancer susceptibility, diagnosis and prognosis, also for
XX selection of treatment, e.g. susceptibility to early-onset familial
XX breast cancer. Gene nm23 may contribute to tumourigenicity and alteration
XX in its regulation may be an early stage in the metastatic cascade.

CC Allelic or homozygous deletion of the gene is detected in some primary
CC tumour cells
XX SQ Sequence 176 AA;
Query Match 100.0%; Score 803; DB 5; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.6e-90;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 25 MANLERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 84
QY 61 FPGLVKYMNSGPPVAMVWVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 85 FPGLVKYMNSGPPVAMVWVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 144
QY 121 DSVKSAEKETSLWFKPEELVDYKSCAHDWVYE 152
Db 145 DSVKSAEKETSLWFKPEELVDYKSCAHDWVYE 176
RESULT 15
AEA90109
ID AEA90109 standard; protein; 151 AA.
XX AC AEA90109;
XX DT 25-AUG-2005 (first entry)
XX DE Human nucleoside diphosphate kinase protein, SEQ ID NO: 1.
XX KW Selectable marker; screening; diagnosis; liver disease; hepatotropic;
KW gastrointestinal disease; liver cirrhosis; liver cancer; cytostatic;
KW neoplasm; antigen; nucleoside diphosphate kinase; enzyme.
XX OS Homo sapiens.
XX PN US2005136489-A1.
XX PD 23-JUN-2005.
XX PF 17-DEC-2004; 2004US-00013684.
XX PR 19-DEC-2003; 2003TW-00136309.
XX PA (INTB-) IND TECHNOLOGY RES INST.
XX PI Tseng T, Cheng P;
XX WPI; 2005-444137/45.
XX New biomarker for liver diseases comprising specific sequences, useful
XX for developing kits for diagnosing liver cirrhosis or liver cancer.
XX Claim 1; SEQ ID NO 1; 40pp; English.
XX The invention relates to novel biomarkers for liver diseases. The
XX invention also relates to the use of an autoantigen screening method to
XX identify biomarkers that can be used in detecting liver diseases such as
XX liver cirrhosis and liver cancer. The present sequence is the human
XX nucleoside diphosphate kinase protein. This sequence is the autoantigen
XX identified from cell lines using sera of patients with liver cirrhosis
XX and liver cancer.
XX SQ Sequence 151 AA;
Query Match 99.4%; Score 798; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.5e-89;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ANLERTFIAIKPDGVQVGLVGEIIKRFQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF 61
|||||

Db	1	ANLERTTFAIKPDGVQRGLVGEIIKRFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPFF	60
Qy	62	PGLVKYMNSGFVAVMWEGNLNVVKTGRVMLGETNPADSKPGTIRGDFCQVGRNIIHGSD	121
Db	61	PGLVKYMNSGFVAVMWEGNLNVVKTGRVMLGETNPADSKPGTIRGDFCQVGRNIIHGSD	120
Qy	122	SVKSAEKEISLWFKPEELVDYKSCAHDWVYE	152
Db	121	SVKSAEKEISLWFKPEELVDYKSCAHDWVYE	151

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Job time : 127.667 secs

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OM protein - protein search, using sw model

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(without alignments)
153.021 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pdb:
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pdb:
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	759	86.6	152	6	US-10-878-556A-49	Sequence 49, Appl
2	729	83.2	152	6	US-10-821-234-1577	Sequence 1577, Ap
3	333.5	38.1	136	7	US-11-055-822-966	Sequence 966, App
4	333.5	38.1	136	7	US-11-055-822-994	Sequence 994, App
5	303	34.6	141	6	US-10-467-657-4110	Sequence 4110, Ap
6	76	8.7	428	6	US-10-763-712A-118	Sequence 118, App
7	73.5	8.4	1144	6	US-10-467-657-1820	Sequence 1820, Ap
8	69.5	7.9	1302	7	US-11-090-439-42	Sequence 42, Appl
9	69	7.9	795	6	US-10-770-726-49	Sequence 49, Appl
10	68	7.8	293	6	US-10-467-657-4834	Sequence 4834, Ap
11	67	7.6	2261	6	US-10-995-561-600	Sequence 600, App
12	66.5	7.6	364	6	US-10-131-826A-342	Sequence 342, App
13	66.5	7.6	364	7	US-11-091-334-2	Sequence 2, Appli
14	66	7.5	428	6	US-10-793-626-2050	Sequence 2050, Ap
15	64	7.3	1101	6	US-10-878-556A-107	Sequence 107, App
16	63.5	7.2	295	7	US-11-143-980-31	Sequence 31, Appl
17	63.5	7.2	347	6	US-10-467-657-6092	Sequence 6092, Ap
18	63.5	7.2	347	6	US-10-467-657-7548	Sequence 7548, Ap
19	63	7.2	366	6	US-10-510-386-42	Sequence 42, Appl
20	62.5	7.1	299	7	US-11-055-822-408	Sequence 408, App
21	62.5	7.1	365	7	US-11-102-978-9	Sequence 9, Appli
22	62.5	7.1	365	7	US-11-080-991-78	Sequence 78, Appl
23	62	7.1	375	7	US-11-051-267-16	Sequence 16, Appl
24	62	7.1	527	6	US-10-821-234-1574	Sequence 1574, Ap
25	61.5	7.0	480	6	US-10-510-386-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-10-878-556A-49
; Sequence 49, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 49
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ndka_human
; DATABASE ENTRY DATE: 1990-04-01
US-10-878-556A-49

Query Match 86.6%; Score 759; DB 6; Length 152;
Best Local Similarity 94.1%; Pred. No. 3.3e-72;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy	15	MANSERTFIAIKPDGVORGLVGEIIRKFEQKQFRLVGLKFLQASEDLKHEHYTDLKDRPF	74
Db	1	MANCERTFIAIKPDGVORGLVGEIIRKFEQKQFRLVGLKFLQASEDLKHEHYTDLKDRPF	60
Qy	75	FTGLVKYHSGPVVAVWVWGLNVKTRVLMGETNPADSKPGTIRGDFCQVGRNIHGS	134
Db	61	FAGLVKYMHSQPVVAVWVWGLNVKTRVLMGETNPADSKPGTIRGDFCQVGRNIHGS	120
Qy	135	DSVKSAREKISLMFQPEELVEYKSCAQNWIYE	166
Db	121	DSVESAEKRIGLWPHPEELVDYTSCAQNWIYE	152

RESULT 2

US-10-821-234-1577
; Sequence 1577, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

```
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1577
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1577

Query Match      83.2%; Score 729; DB 6; Length 152;
Best Local Similarity 90.1%; Pred. No. 4.3e-69;
Matches 137; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 15 MANSRTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MANLRTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKHQHYIDLKDRPF 60

QY 75 FTGLVKYMSGPPVAMVWGLNVVKTGRVMLGTNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FPLGLVKYMSGPPVAMVWGLNVVKTGRVMLGTNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 135 DSVKSAEKETSLWFOPEELVEYKSCAQNWIYE 166
Db 121 DSVKSAEKETSLWFKPEELVDYKSCAHDWVYE 152
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RESULT 3
US-11-055-822-966
; Sequence 966, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habershauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 966
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-966
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Query Match      38.1%; Score 333.5; DB 7; Length 136;
Best Local Similarity 49.2%; Pred. No. 4.9e-28;
Matches 65; Conservative 24; Mismatches 42; Indels 1; Gaps 1;

QY 18 SERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 77
Db 2 TERTLILIKPDGVTVNGHVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 61

QY 78 LVKYMHSQPVVAMVWGLNVVKTGRVMLGTNP-ADSKPGTIRGDFCIQVGRNIHGS 136
Db 62 LVEFITSAPLIAGIVEGERAIDAWQLAGTDPVAKATPGTIRGDFALTUVGENVHGS 121

QY 137 VKSAEKEISLWF 148
Db 122 PESAREEISLWF 133

RESULT 4
US-11-055-822-994
; Sequence 994, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habershauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 994
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-994

Query Match      38.1%; Score 333.5; DB 7; Length 136;
Best Local Similarity 49.2%; Pred. No. 4.9e-28;
Matches 65; Conservative 24; Mismatches 42; Indels 1; Gaps 1;

QY 18 SERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 77
Db 2 TERTLILIKPDGVTVNGHVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 61

QY 78 LVKYMHSQPVVAMVWGLNVVKTGRVMLGTNP-ADSKPGTIRGDFCIQVGRNIHGS 136
Db 62 LVEFITSAPLIAGIVEGERAIDAWQLAGTDPVAKATPGTIRGDFALTUVGENVHGS 121

QY 137 VKSAEKEISLWF 148
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Query Match 8.7%; Score 76; DB 6; Length 428;
Best Local Similarity 21.5%; Pred. No. 1.2;


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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 342
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-342

Query Match      7.6%; Score 66.5; DB 6; Length 364;
Best Local Similarity 24.2%; Pred. No. 9.7;
Matches 48; Conservative 23; Mismatches 70; Indels 57; Gaps 11;

QY  3 QPAVKPCHLKGTMANSERTFIAIKPDGVQR-----GLVGEIIRKFEQKGFRLVGLKF 54
Db  45 QPV--PVILKKIFQDRE-----AAATTGVSRLDLCYVKELGVRGNVRLFLPDQGFLLYPKKI 98
QY  55 LQASEDLLKEHYTDL---KORPFFT-----GLVKYMHSGPVVAMVWEGNLNVVKTGRV 103
Db  99 SQASSCLQKLLYFNLSAIREQLTLAQLGLDLPNSYNLGPELEL---ALFLVQEPHV 155
QY  104 MLGETNPADSKPGTIRGDFCIQVGRNIH-----GSDSVKSAEKEISLW----- 147
Db  156 W-QGTTKPKGMFVLRS---VPWPQGAHVHNLVDVAKDNDNPRKNFGLFLEILVKESDRD 211
QY  148 ----FOPEELVEYKSCAQ 161
Db  212 SGVNFQPED-----TCAR 224

RESULT 13
US-10-793-626-2050
; Sequence 2050, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2050
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2050

Query Match      7.5%; Score 66; DB 6; Length 428;
Best Local Similarity 25.5%; Pred. No. 14;
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US-11-091-334-2
; Sequence 2, Application US/11091334
; Publication No. US20050244867A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, et al.
; TITLE OF INVENTION: Growth Factor HTT36
; FILE REFERENCE: PF230P1
; CURRENT APPLICATION NUMBER: US/11/091,334
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/557,393
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: 10/117,178
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 09/357,905
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 08/827,336
; PRIOR FILING DATE: 1997-03-26
; PRIOR APPLICATION NUMBER: 60/014,098
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-334-2

Query Match      7.6%; Score 66.5; DB 7; Length 364;
Best Local Similarity 24.2%; Pred. No. 9.7;
Matches 48; Conservative 23; Mismatches 70; Indels 57; Gaps 11;

QY  3 QPAVKPCHLKGTMANSERTFIAIKPDGVQR-----GLVGEIIRKFEQKGFRLVGLKF 54
Db  45 QPV--PVILKKIFQDRE-----AAATTGVSRLDLCYVKELGVRGNVRLFLPDQGFLLYPKKI 98
QY  55 LQASEDLLKEHYTDL---KORPFFT-----GLVKYMHSGPVVAMVWEGNLNVVKTGRV 103
Db  99 SQASSCLQKLLYFNLSAIREQLTLAQLGLDLPNSYNLGPELEL---ALFLVQEPHV 155
QY  104 MLGETNPADSKPGTIRGDFCIQVGRNIH-----GSDSVKSAEKEISLW----- 147
Db  156 W-QGTTKPKGMFVLRS---VPWPQGAHVHNLVDVAKDNDNPRKNFGLFLEILVKESDRD 211
QY  148 ----FOPEELVEYKSCAQ 161
Db  212 SGVNFQPED-----TCAR 224

RESULT 14
US-10-793-626-2050
; Sequence 2050, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2050
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2050

Query Match      7.5%; Score 66; DB 6; Length 428;
Best Local Similarity 25.5%; Pred. No. 14;
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:38:19 ; Search time 117.453 Seconds
(without alignments)
590.532 Million cell updates/sec

Title: US-10-074-694-3

Perfect score: 876

Sequence: 1 OSQPAVKPCHLKGTMANSE.....WFQPEELVEYKSCAQNWIIYE 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:**
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:**
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:**
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 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	876	100.0	166	5	US-10-732-923-13110
2	798	91.1	152	3	US-09-791-118A-2
3	798	91.1	152	5	US-10-732-923-13111
4	794	90.6	176	5	US-10-732-923-13112
5	794	90.6	178	3	US-09-833-790-426
6	794	90.6	180	5	US-10-732-923-13340
7	794	90.6	180	6	US-11-013-684-2
8	794	90.6	180	6	US-11-037-713-42
9	779	88.9	152	5	US-10-732-923-13126
10	774.5	88.4	177	4	US-10-288-798-19
11	774.5	88.4	177	4	US-10-362-892-19
12	774.5	88.4	177	5	US-10-732-923-13342
13	759	86.6	152	3	US-09-791-118A-1
14	759	86.6	152	4	US-10-232-188-4
15	759	86.6	152	4	US-10-133-628-11
16	759	86.6	152	5	US-10-370-715B-110
17	759	86.6	152	5	US-10-732-923-13341
18	755	86.2	152	5	US-10-732-923-13355
19	754	86.1	152	4	US-10-133-628-2
20	754	86.1	152	5	US-10-732-923-13353
21	752	85.8	152	4	US-10-133-628-21
22	749	85.5	151	5	US-10-732-923-13354
23	747	85.3	152	4	US-10-133-628-3
24	732.5	83.6	153	5	US-10-732-923-13132
25	729	83.2	152	3	US-09-791-118A-3
26	729	83.2	152	4	US-10-232-188-5
27	729	83.2	152	4	US-10-133-628-12

28	729	83.2	152	4	US-10-440-464-90	Sequence 90, Appl
29	729	83.2	152	5	US-10-732-923-13345	Sequence 13345, A
30	725	82.8	190	4	US-10-363-829-352	Sequence 352, App
31	724	82.6	151	5	US-10-732-923-13346	Sequence 13346, A
32	724	82.6	151	6	US-11-013-684-1	Sequence 1, Appli
33	724	82.6	152	4	US-10-133-628-4	Sequence 4, Appli
34	720	82.2	152	5	US-10-732-923-13127	Sequence 13127, A
35	719	82.1	152	3	US-09-791-118A-4	Sequence 4, Appli
36	719	82.1	152	4	US-10-116-275-332	Sequence 332, App
37	719	82.1	152	5	US-10-732-923-13113	Sequence 13113, A
38	717	81.8	152	4	US-10-133-628-5	Sequence 5, Appli
39	714	81.5	153	5	US-10-732-923-13320	Sequence 13320, A
40	713	81.4	152	5	US-10-732-923-13128	Sequence 13128, A
41	712	81.3	153	5	US-10-732-923-13336	Sequence 13336, A
42	710	81.1	153	5	US-10-732-923-13334	Sequence 13334, A
43	704	80.4	153	5	US-10-732-923-13117	Sequence 13117, A
44	699	79.8	153	5	US-10-732-923-13315	Sequence 13315, A
45	696	79.5	152	5	US-10-732-923-13119	Sequence 13119, A

ALIGNMENTS

RESULT 1
US-10-732-923-13110
; Sequence 13110, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13110
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-13110

Query Match 100.0%; Score 876; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.3e-88;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	OSQPAVKPCHLKGTMANSE	FTFAIKPDGVQRLVGEIIKRF	EKGFRVLGLKFLQASED	60
Db	1	OSQPAVKPCHLKGTMANSE	FTFAIKPDGVQRLVGEIIKRF	EKGFRVLGLKFLQASED	60
Qy	61	LLKEHYTDLKDRPFF	TGLVKYMHSGPVVAMVW	EGLNVVKTGRVLMGETNP	ADSKPGTIRG 120
Db	61	LLKEHYTDLKDRPFF	TGLVKYMHSGPVVAMVW	EGLNVVKTGRVLMGETNP	ADSKPGTIRG 120
Qy	121	DFCIQVGRNIHGS	DSVSKAEKISLWFQPEEL	VEYKSCAQNWIIYE	166
Db	121	DFCIQVGRNIHGS	DSVSKAEKISLWFQPEEL	VEYKSCAQNWIIYE	166

RESULT 2
US-09-791-118A-2
; Sequence 2, Application US/09791118A
; Patent No. US20020034741A1
; GENERAL INFORMATION:
; APPLICANT: Werner, Sabine
; APPLICANT: Braun, Susanne
; APPLICANT: Penzberg, Jorn-Peter
; APPLICANT: Goppelt, Andreas
; APPLICANT: Regenbogen, Johannes
; TITLE OF INVENTION: Use of polypeptides or nucleic acids
; TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or
; TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for
; TITLE OF INVENTION: the identification of pharmacologically

```
; TITLE OF INVENTION: active substances
; FILE REFERENCE: 50125/012002
; CURRENT APPLICATION NUMBER: US/09/791.118A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/199,312
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: DE 100 08 330.7
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-118A-2
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Query Match 91.1%; Score 798; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 MANSERTFIAIKDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60
QY 75 FTGLVKYMHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCICQVGRNIHGS 134
Db 61 FTGLVKYMHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCICQVGRNIHGS 120
QY 135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
Db 121 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 152
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RESULT 3

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US-10-732-923-13111
; Sequence 13111, Application US/10732923
; Publication No. US20050108791A1
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; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13111
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-13111
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Query Match 91.1%; Score 798; DB 5; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 MANSERTFIAIKDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60
QY 75 FTGLVKYMHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCICQVGRNIHGS 134
Db 61 FTGLVKYMHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCICQVGRNIHGS 120
QY 135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
Db 121 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 152
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RESULT 4

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US-10-732-923-13112
; Sequence 13112, Application US/10732923
; Publication No. US20050108791A1
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; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13112
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-13112
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Query Match 90.6%; Score 794; DB 5; Length 176;
Best Local Similarity 91.5%; Pred. No. 4.1e-79;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY 3 QPAVKPCHLKGTMANSERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDL 62
Db 13 QPEFKPKQLEGTMANCERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDL 72
QY 63 KEHYTDLKDRPFPTGLVKYMHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDF 122
Db 73 KEHYVDLKDPPFAGLVKYMHSFPVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDF 132
QY 123 CIOVGRNIHGS DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
Db 133 CIOVGRNIHGS DSVKSAEKEISLWFPHPELVDTYTS CAQNWIYE 176
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RESULT 5

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US-09-833-790-426
; Sequence 426, Application US/09833790
; Patent No. US20020068288A1
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; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Ligu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-426
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Query Match 90.6%; Score 794; DB 3; Length 178;
Best Local Similarity 91.5%; Pred. No. 4.1e-79;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY 3 QPAVKPCHLKGTMANSERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDL 62
Db 15 QPEFKPKQLEGTMANCERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVGLKFLQASEDL 74
QY 63 KEHYTDLKDRPFPTGLVKYMHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDF 122
Db 75 KEHYVDLKDPPFAGLVKYMHSFPVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDF 134
QY 123 CIOVGRNIHGS DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
Db 135 CIOVGRNIHGS DSVKSAEKEISLWFPHPELVDTYTS CAQNWIYE 178
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; Sequence 42, Application US/11037713
; Publication No. US20050221398A1
; GENERAL INFORMATION:
; APPLICANT: JACQUEMIER, JOCELYNE
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: DEBONO, STEPHANE
; APPLICANT: TAGETT, REBECCA
; TITLE OF INVENTION: PROTEIN EXPRESSION PROFILING AND BREAST CANCER
; FILE REFERENCE: 1016-R-04(B)
; CURRENT APPLICATION NUMBER: US/11/037,713
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: 60/537,412
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 42
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-713-42

Query Match          90.6%; Score 794; DB 6; Length 180;
Best Local Similarity 91.5%; Pred.No. 4.2e-79;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      3 QPAVKPCHLKGTWANSERTFIAIKPDGVQRGLVGEIHKRFEQGFRVLVGKFLQASEDLLL 62
DB      17 QPEFKPKLEGTWANCERTFIAIKPDGVRQLVGEIIKRFEQGFRVLVGKFLMQASEDLL 76

QY      63 KEHYDLDKPFPFTGLVKVMHSGPVVAMWEGLNVKTGRVMLGETNPADSKPGTIRGDF 122
DB      77 KEHYVDLPDPFFAGLVKYMHSGPVVAMWEGLNVKTGRVMLGETNPADSKPGTIRGDF 136

QY      123 CIOVGNRIHGSDSVSAKEEISLMFOPELVEYSKAQNWIYE 166
DB      137 CIOVGNRIHGSDSVSAKEEGILGFHPHELVDYTSCAQNWIE 180


RESULT 9
US-10-732-923-13126
; Sequence 13126, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13126
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13126

Query Match          88.9%; Score 779; DB 5; Length 152;
Best Local Similarity 96.7%; Pred.No. 1.5e-77;
Matches 147; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      15 MANSERTFIAIKPDGVRQLVGEIHKRFEQGFRVLVGKFLQASEDLLEKHYYIDLKDPPF 74
DB      1 MANSERTFIAIKPDGVRQLVGEIHKRFEQGFRVLVGKFLQASEDLLEKHYYIDLKDPPF 60

QY      75 FTGLVKTMHSMPVVAMWEGLNVKTGRVMLGETNPADSKPGTIRGDPCIOVGRNIHGS 134
DB      61 FSGLVKTMHSMPVVAMWEGLNVKTGRVMLGETNPADSKPGTIRGDPCIOVGRNIHGS 120

QY      135 DSVSAAKETLSLFOPBELVEYSKAQNWIYE 166
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Db 121 DSVSAEKEISLWFPPELVYKSCAQNIYE 152
; Sequence 19, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Dannel B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: THORNTON, Michael; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7274927CD1
US-10-288-798-19
Query Match 88.4%; Score 774.5; DB 4; Length 177;
Best Local Similarity 90.2%; Pred. No. 5.8e-77;
Matches 147; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 4 PAVKPCHLKGTWANSERTFTAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLK 63
Db 16 PPISCD-TGTWANCERTFTAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLK 74
QY 64 EHYTDLKDRPFFGLVKYMHSGVPVAMWEGLVNVTGRVMLGETNPADSKPGTIRGDFC 123
Db 75 EHYVDLKDPRFFAGLVKYMHSGLVAMWEGLVNVTGRVMLGETNPADSKPGTIRGDFC 134
QY 124 IQVGRNIHGSDSVSAEKEISLWFPPELVYKSCAQNIYE 166
Db 135 IQVGRNIHGSDSVSAEKEISLWFPPELVYKSCAQNIYE 177

RESULT 12
US-10-732-923-13342
; Sequence 13342, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D

Db 121 DSVSAEKEISLWFPPELVYKSCAQNIYE 152
; Sequence 19, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Dannel B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: THORNTON, Michael; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7274927CD1
US-10-288-798-19
Query Match 88.4%; Score 774.5; DB 4; Length 177;
Best Local Similarity 90.2%; Pred. No. 5.8e-77;
Matches 147; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 4 PAVKPCHLKGTWANSERTFTAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLK 63
Db 16 PPISCD-TGTWANCERTFTAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLK 74
QY 64 EHYTDLKDRPFFGLVKYMHSGVPVAMWEGLVNVTGRVMLGETNPADSKPGTIRGDFC 123
Db 75 EHYVDLKDPRFFAGLVKYMHSGLVAMWEGLVNVTGRVMLGETNPADSKPGTIRGDFC 134
QY 124 IQVGRNIHGSDSVSAEKEISLWFPPELVYKSCAQNIYE 166
Db 135 IQVGRNIHGSDSVSAEKEISLWFPPELVYKSCAQNIYE 177

RESULT 11
US-10-362-892-19
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; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13342
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-13342

Query Match 88.4%; Score 774.5; DB 5; Length 177;
Best Local Similarity 90.2%; Pred. No. 5.8e-77;
Matches 147; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
Qy 4 PAVKPCHLKGTMANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLK 63
Db 16 PPISSCD-TGTMANCERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLK 74
Qy 64 EHYTDLKDRPFFGLVKYMHSGPVVAMVWGLNVKTRVLMGETNPADSKPGTIRGDFC 123
Db 75 EHYVDLKDORPFFGLVKYMHSGPVVAMVWGLNVKTRVLMGETNPADSKPGTIRGDFC 134
Qy 124 IQVGRNIHGS DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 166
Db 135 IQVGRNIHGS DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 177

RESULT 13
US-09-791-118A-1
; Sequence 1, Application US/09791118A
; Patent No. US20020034741A1
; GENERAL INFORMATION:
; APPLICANT: Werner, Sabine
; APPLICANT: Braun, Susanne
; APPLICANT: Penzberg, Jorn-Peter
; APPLICANT: Goppelt, Andreas
; APPLICANT: Regenbogen, Johannes
; TITLE OF INVENTION: Use of polypeptides or nucleic acids
; TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or
; TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for
; TITLE OF INVENTION: the identification of pharmacologically
; TITLE OF INVENTION: active substances
; FILE REFERENCE: 50125/012002
; CURRENT APPLICATION NUMBER: US/09/791,118A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/199,312
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: DE 100 08 330.7
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-118A-1

Query Match 86.6%; Score 759; DB 3; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-75;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 15 MANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60
Qy 75 FTGLVKYMHSGPVVAMVWGLNVKTRVLMGETNPADSKPGTIRGDFC IQVGRNIHGS 134
Db 61 FAGLVKYMHS GPVAVMWGLNVKTRVLMGETNPADSKPGTIRGDFC IQVGRNIHGS 120
Qy 135 DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 166

Db 121 DSVESAKEISLWFOPEELVEYKSCAQNIWE 152
RESULT 14
US-10-232-188-4
; Sequence 4, Application US/10232188
; Publication No. US20030022306A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,188
; FILING DATE: 28-Aug-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 468542
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-232-188-4

Query Match 86.6%; Score 759; DB 4; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-75;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 15 MANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60
Qy 75 FTGLVKYMHSGPVVAMVWGLNVKTRVLMGETNPADSKPGTIRGDFC IQVGRNIHGS 134
Db 61 FAGLVKYMHS GPVAVMWGLNVKTRVLMGETNPADSKPGTIRGDFC IQVGRNIHGS 120
Qy 135 DSVKSAEKEISLWFOPEELVEYKSCAQNIWE 166
Db 121 DSVESAKEISLWFOPEELVEYKSCAQNIWE 152
RESULT 15
US-10-133-628-11
; Sequence 11, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:59 ; Search time 31.5472 Seconds
(without alignments)
398.346 Million cell updates/sec

Title: US-10-074-694-5

Perfect score: 803

Sequence: 1 MANLERTFAIKDGVQVGL.....WFKPELVYDKSCAHDWVYE 152

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	100.0	152	1	US-08-713-825-5
2	803	100.0	152	2	US-09-199-842-5
3	803	100.0	152	2	US-09-335-948-1
4	803	100.0	152	2	US-09-460-532-5
5	803	100.0	152	2	US-09-538-092-987
6	803	100.0	176	2	US-09-335-948-2
7	803	100.0	176	2	US-07-806-932B-3
8	720	89.7	152	1	US-08-713-825-4
9	720	89.7	152	2	US-09-199-842-4
10	720	89.7	152	2	US-09-335-948-4
11	720	89.7	152	2	US-09-460-532-4
12	720	89.7	152	2	US-09-538-092-933
13	720	89.7	184	2	US-09-335-948-5
14	720	89.7	184	2	US-07-806-932B-1
15	594	74.0	117	2	US-09-513-999C-5323
16	536.5	66.8	168	1	US-08-667-023-2
17	536.5	66.8	168	1	US-08-713-825-3
18	536.5	66.8	168	2	US-09-199-842-3
19	536.5	66.8	168	2	US-09-460-532-3
20	533	66.4	151	2	US-09-183-861-20
21	533	66.4	151	2	US-09-022-765-20
22	533	66.4	151	2	US-09-551-974A-20
23	533	66.4	151	2	US-09-565-501A-20
24	533	66.4	151	2	US-09-639-206A-20
25	533	66.4	151	2	US-09-874-923-20
26	533	66.4	151	2	US-08-798-841-20
27	519	64.6	153	2	US-09-248-796A-18029

Sequence 491, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 823, Appli
Sequence 59, Appli
Sequence 4, Appli
Sequence 3216, Appli
Sequence 91, Appli
Sequence 3639, Appli
Sequence 3645, Appli
Sequence 1, Appli
Sequence 10381, A
Sequence 6000, Appli
Sequence 2, Appli
Sequence 7960, Appli
Sequence 3095, Appli

ALIGNMENTS

RESULT 1
US-08-713-825-5
; Sequence 5, Application US/08713825
; Patent No. 5874285
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,825
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 127983
US-08-713-825-5

Query Match 100.0%; Score 803; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 2
US-09-199-842-5
; Sequence 5, Application US/09199842
; Patent No. 6087125
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/199,842
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: 08/713,825
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 127983
; US-09-199-842-5
Query Match 100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 3
US-09-335-948-1
; Sequence 1, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; FILE REFERENCE: 14014.0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-335-948-1
Query Match 100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPPVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Db 61 FPGLVKYMNSGPPVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 4
US-09-460-532-5
; Sequence 5, Application US/09460532
; Patent No. 6486300
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 13-Dec-1999
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/199,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/713,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 152 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 127983
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-460-532-5

Query Match      100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152

RESULT 5
US-09-538-092-987
; Sequence 987, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqformatter Version 0.9
; SEQ ID NO 987
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P22392
US-09-538-092-987

Query Match      100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152

RESULT 6
US-09-335-948-2
; Sequence 2, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; FILE REFERENCE: 14014, 0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-335-948-2

Query Match      100.0%; Score 803; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.9e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 25 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 84
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 85 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 144
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 145 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 176

RESULT 7
US-07-806-932B-3
; Sequence 3, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:
; APPLICANT: KING, ET AL.
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
; TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI & STEWART
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
```

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; APPLICATION NUMBER: US/09/199,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/713,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 152 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 127983
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-460-532-5

Query Match      100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152

RESULT 6
US-09-335-948-2
; Sequence 2, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; FILE REFERENCE: 14014, 0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-335-948-2

Query Match      100.0%; Score 803; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.9e-91;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 25 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGRFLVAMKFLRASEEHLKQHYIDLKDRPF 84
Qy 61 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Db 85 FPGLVKYMNSGPVVAMVWEGVLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 144
Qy 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 152
Db 145 DSVKSAEKEISLWFKPEELVDYKSCAHDWYVE 176

RESULT 7
US-07-806-932B-3
; Sequence 3, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:
; APPLICANT: KING, ET AL.
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
; TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI & STEWART
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
```


TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 468542
US-09-199-842-4

Query Match 89.7%; Score 720; DB 2; Length 152;
Best Local Similarity 88.2%; Pred. No. 3.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANCERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFMQASEDLKHEHYVDLDRPF 60
Qy 61 FPGLVKYNMNSGPPVAMVWEGNLVVKTRVLMGETNPADSKPTGIRGDFCIQVGRNIHGS 120
Db 61 FAGLVKYMHSPPVAMVWEGNLVVKTRVLMGETNPADSKPTGIRGDFCIQVGRNIHGS 120
Qy 121 DSVSAEKEISLWFKPELVDYKSCAHDWVE 152
Db 121 DSVSAEKEISLWFKPELVDYTSCAQNWIYE 152

RESULT 10

US-09-335-948-4
; Sequence 4, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; FILE REFERENCE: 14014.0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 152
; TYPE: PPT
; ORGANISM: Homo Sapiens
US-09-335-948-4

Query Match 89.7%; Score 720; DB 2; Length 152;
Best Local Similarity 88.2%; Pred. No. 3.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANCERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFMQASEDLKHEHYVDLDRPF 60
Qy 61 FPGLVKYNMNSGPPVAMVWEGNLVVKTRVLMGETNPADSKPTGIRGDFCIQVGRNIHGS 120
Db 61 FAGLVKYMHSPPVAMVWEGNLVVKTRVLMGETNPADSKPTGIRGDFCIQVGRNIHGS 120
Qy 121 DSVSAEKEISLWFKPELVDYKSCAHDWVE 152

Db 121 DSVSAEKEISLWFKPELVDYTSCAQNWIYE 152

RESULT 11

US-09-460-532-4
; Sequence 4, Application US/09460532
; Patent No. 6486300
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,532
; FILING DATE: 13-Dec-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/713,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 468542
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-460-532-4

Query Match 89.7%; Score 720; DB 2; Length 152;
Best Local Similarity 88.2%; Pred. No. 3.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MANLERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 1 MANCERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFMQASEDLKHEHYVDLDRPF 60
Qy 61 FPGLVKYNMNSGPPVAMVWEGNLVVKTRVLMGETNPADSKPTGIRGDFCIQVGRNIHGS 120
Db 61 FAGLVKYMHSPPVAMVWEGNLVVKTRVLMGETNPADSKPTGIRGDFCIQVGRNIHGS 120
Qy 121 DSVSAEKEISLWFKPELVDYKSCAHDWVE 152
Db 121 DSVSAEKEISLWFKPELVDYTSCAQNWIYE 152

RESULT 12

US-09-538-092-933
; Sequence 933, Application US/09538092

```
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; APPLICANT: Mansfield, Traci A.
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 933
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number PI5531
US-09-538-092-933

Query Match          89.7%; Score 720; DB 2; Length 152;
Best Local Similarity 88.2%; Pred.No.3.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY      1   MANLERTFIAIKPDGVORGVLGEITIKPEQGFLVAMKFLRASEEHLKHVIDLKDPFF    60
       ||| | | | | | | | | | | | | | | | | | | | | : | | | | | | | | |
Db      1   MANCERTFIAIKPDGVORGVLGEITIKPEQGFLVGLKFMAQSEDLKKHEYVDLKDPFF    60
       ||| | | | | | | | | | | | | | | | | | | | | : | | | | | | | | |

QY     61   FPGLVKYMNSGPPVVAMWEGNLNVVKTKGRVLMGETNPNADSKPTGTIRGDFCIQVGNNIHGS    120
       ||| | | | | | | | | | | | | | | | | | | | | : | | | | | | | | |
Db     61   FAGLVKYMNSGPPVVAMWEGNLNVVKTKGRVLMGETNPNADSKPTGTIRGDFCIQVGNNIHGS    120
       ||| | | | | | | | | | | | | | | | | | | | | : | | | | | | | | |

QY    121   DSVKSAREKETLSLFKPDELVDYSKAHDWWEY    152
       ||| | | | | | | | | | | | | | | | | | | | | : | | | | | | | | |
Db    121   DSVESAEKETGLWFHPDELDVTYSQAQNWIYE    152
       ||| | | | | | | | | | | | | | | | | | | | | : | | | | | | | | |
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RESULT 13
US-09-335-948-5
; Sequence 5, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; FILE REFERENCE: 14014. 0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-335-948-5

Query Match      89.7%; Score 720; DB 2; Length 184;
Best Local Similarity 88.2%; Pred. No. 4.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy 1 MANLERTFIAIKPDGVORGLVGEIILKKEFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 33 MANCERTFIAIKPDGVORGLVGEIILKKEFEQKGFRLVGLKFMQASEDLKKEHYVDLKDREF 92
Qy 61 FPGVLKYMNSGPPVVMYMWEGVLNVKTVGRVLMGETNPADSKPGTIRGDFCIVQGRNIIHGS 120
Db 93 FAGLVKMHSGPPVVMYMWEGVLNVKTVGRVLMGETNPADSKPGTIRGDFCIVQGRNIIHGS 152
Qy 121 DSVKSAKEKISLMFKPEELVDYKSCAHDWYVE 152
Db 153 DSVESAKEIGLWHPPELVDTYTSCAQNIWE 184

RESULT 14
US-07-806-932B-1
; Sequence 1, Application US/07806932B
; Patent No. 6421836
; GENERAL INFORMATION:
; APPLICANT: KING, ET AL.
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
; TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI & STEWART
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/806,932B
; FILING DATE: 11 december 1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,801
; FILING DATE: 18 october 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: CAPELLO, SUSAN A.
; REGISTRATION NUMBER: 34,560
; REFERENCE/DOCKET NUMBER: 469200-72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 AMINO ACID RESIDUES
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE: HUMAN NM 23-H28
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION: 1: FROM -32 TO 152
US-07-806-932B-1

Query Match 89.7%; Score 720; DB 2; Length 184;
Best Local Similarity 88.2%; Pred. No. 4.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels 0; Gaps 0

Qy 1 MANLERTFIAIKPDGVORGLVGEIILKKEFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
Db 33 MANCERTFIAIKPDGVORGLVGEIILKKEFEQKGFRLVGLKFMQASEDLKKEHYVDLKDREF 92
Qy 61 FPGVLKYMNSGPPVVMYMWEGVLNVKTVGRVLMGETNPADSKPGTIRGDFCIVQGRNIIHGS 120

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Db	93	FAGLVKYMHSQVVAAMVWEGVLNVYKTRGVLGETNPADSKPGTIRGDFCIQVGRNIHGS	152
Qy	121	DSVKSAREKISLWFPKPEELVDYKSCADHWYE	152
Db	153	DSVGSAREKIGLWFPKPEELVDYTSQAQNWIIYE	184

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RESULT 15
US-09-513-999C-5323
; Sequence 5323, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5323
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5323

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	Query Match	74.0%; Score 594; DB 2; Length 117;
	Best Local Similarity	99.1%; Pred. No. 9.7e-66;
	Matches 116; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MANLERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKHQYIDLKDRPF	60
Dd	1 MANLERTFIAIKPDGVORGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKHQYIDLKDRPF	60
Qy	61 FPGILVKYMNSGPVVAMYWEGLNVVKTGRVLMGETNPADSKPGTITRGFCIQVGNII	117
Dd	61 FPGILVKYMNSGPVVAMYREGLVNVTGRVLMGETNPADSKPGTITRGFCIQVGNII	117

Search completed: December 16, 2005, 16:38:13
Job time : 32.5472 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:59 ; Search time 34.4528 Seconds
(without alignments)
398.346 Million cell updates/sec

Title: US-10-074-694-3

Perfect score: 876

Sequence: 1 QSQPAVKCHLKGTMANSE.....WFOPELVEYKSCAQNWYIE 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	794	90.6	184	2	US-09-335-948-5
2	794	90.6	184	2	US-07-806-932B-1
3	759	86.6	152	1	US-08-713-825-4
4	759	86.6	152	2	US-09-199-842-4
5	759	86.6	152	2	US-03-335-948-4
6	759	86.6	152	2	US-03-460-532-4
7	759	86.6	152	2	US-09-538-092-933
8	734	83.8	176	2	US-09-335-948-2
9	734	83.8	176	2	US-07-806-932B-3
10	729	83.2	152	1	US-08-713-825-5
11	729	83.2	152	2	US-03-199-842-5
12	729	83.2	152	2	US-09-335-948-1
13	729	83.2	152	2	US-09-460-532-5
14	729	83.2	152	2	US-09-538-092-987
15	547.5	62.5	168	1	US-08-667-023-2
16	547.5	62.5	168	1	US-08-713-825-3
17	547.5	62.5	168	2	US-09-199-842-3
18	547.5	62.5	168	2	US-09-460-532-3
19	542	61.9	117	2	US-09-513-999C-5323
20	531	60.6	153	2	US-09-248-796A-18029
21	526	60.0	151	2	US-09-183-861-20
22	526	60.0	151	2	US-09-022-765-20
23	526	60.0	151	2	US-09-551-974A-20
24	526	60.0	151	2	US-09-565-501A-20
25	526	60.0	151	2	US-09-639-206A-20
26	526	60.0	151	2	US-09-874-923-20
27	526	60.0	151	2	US-08-798-841-20

28	492	56.2	153	2	US-09-538-092-491	Sequence 491, App
29	481	54.9	187	1	US-08-713-825-1	Sequence 1, Appli
30	481	54.9	187	2	US-09-199-842-1	Sequence 1, Appli
31	481	54.9	187	2	US-09-460-532-1	Sequence 1, Appli
32	481	54.9	187	2	US-09-538-092-823	Sequence 823, App
33	472	53.9	158	2	US-09-443-184-59	Sequence 59, Appli
34	466	53.2	231	2	US-10-227-035-4	Sequence 4, Appli
35	433	49.4	159	2	US-09-134-001C-3216	Sequence 3216, Ap
36	394	45.0	161	2	US-09-358-972-91	Sequence 91, Appli
37	394	45.0	161	2	US-09-790-417-91	Sequence 91, Appli
38	348	39.7	137	2	US-09-583-110-3639	Sequence 3639, Ap
39	348	39.7	148	2	US-09-107-433-3645	Sequence 3645, Ap
40	328	37.4	154	2	US-09-107-532A-6000	Sequence 6000, Ap
41	320	36.5	145	2	US-09-937-296-1	Sequence 1, Appli
42	320	36.5	145	2	US-09-902-540-10381	Sequence 10381, A
43	318	36.3	145	2	US-09-937-296-2	Sequence 2, Appli
44	308.5	35.2	200	2	US-09-252-991A-22989	Sequence 22989, A
45	307	35.0	153	2	US-09-328-352-7960	Sequence 7960, Ap

ALIGNMENTS

RESULT 1
US-09-335-948-5
; Sequence 5, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; FILE REFERENCE: 14014.0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-335-948-5

Query Match	90.6%	Score 794;	DB 2;	Length 184;
Best Local Similarity	91.5%	Pred. No. 2.4e-85;		
Matches 150;	Conservative 4;	Mismatches 10;	Indels 0;	Gaps 0;
Qy	3	QPAVKCHLKGTMANSERTFIAIKPDGVQRLVGEIIRKFEQKGRVLVGLKFLQASDLL	62	
Db	21	QPQFKPKQLEGTWANCERTFIAIKPDGVQRLVGEIIRKFEQKGRVLVGLKFLQASDLL	80	
Qy	63	KEHYTLKORPFTGLVKYMHSGPVVAMWEGVLNVTGRVMLGETNPADSKPGTIRGDF	122	
Db	81	KEHYVDLKDRPFFAGLVKYMHSGLVAMWEGVLNVTGRVMLGETNPADSKPGTIRGDF	140	
Qy	123	CIOVGRNIHGSVSVAEKEISLWFOPELVEYKSCAQNWYIE	166	
Db	141	CIOVGRNIHGSVSVAEKEISLWFOPELVEYKSCAQNWYIE	184	

RESULT 2
US-07-806-932B-1
; Sequence 1, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:

APPLICANT: KING, ET AL.
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: CAPELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI & STEWART
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 AMINO ACID RESIDUES
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE: HUMAN NM 23-H28
PUBLICATION INFORMATION:
PUBLICATION INFORMATION: 1: FROM -32 TO 152
US-07-806-932B-1

Query Match 90.6%; Score 794; DB 2; Length 184;
Best Local Similarity 91.5%; Pred. No. 2.4e-85;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 QPAVKPCHLKGTMANSERTFAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 62
DB 21 QPQFKPKQLSGTMANCERTFAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLL 80
QY 63 KEHYTDLKDPPFTGLVKYMHSGPVVAMWVGLNVVKTGRVLMGETNPADSKPGTIRGDF 122
DB 81 KEHYVDLKDPPFTAGLVKYMHSQPVVAMWVGLNVVKTGRVLMGETNPADSKPGTIRGDF 140
QY 123 CIQVGRNIHGSVSKSAEKEISLWFOPELVEYKSCAQNIYE 166
DB 141 CIQVGRNIHGSVSKSAEKEISLWFOPELVEYKSCAQNIYE 184

RESULT 3
US-08-713-825-4
Sequence 4, Application US/08713825
Patent No. 5874285
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 468542
US-08-713-825-4

Query Match 86.6%; Score 759; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 15 MANSERTFAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLLKEHYTDLKDPPF 74
DB 1 MANSERTFAIKPDGVQVGLVGEIIRKFEQKGFRLVGLKFLQASEDLLKEHYVDLKDPPF 60
QY 75 FTGLVKYMHSGPVVAMWVGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
DB 61 FAGLVKYMHSQPVVAMWVGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 135 DSVKSAEKEISLWFOPELVEYKSCAQNIYE 166
DB 121 DSVKSAEKEISLWFOPELVEYKSCAQNIYE 152

RESULT 4
US-09-199-842-4
Sequence 4, Application US/09199842
Patent No. 6087125
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,842
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,825
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 468542
; US-09-199-842-4

Query Match      86.6%; Score 759; DB 2; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60

QY 75 FTGLVKYMHSGPVVAMVWEGNLVVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FAGLVKYMHSQPVVAMVWEGNLVVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 135 DSVKSAKEISLWFQPEELVEYKSCAQNWIYE 166
Db 121 DSVESAKEISLWFHPPELVDTYTSCAQNWIYE 152

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RESULT 5
US-09-335-948-4
; Sequence 4, Application US/09335948
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; FILE REFERENCE: 14014.0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; PRIOR FILING DATE: 1999-06-18
; PRIOR FILING DATE: 1995-06-07
; PRIOR FILING DATE: 1991-12-11
; PRIOR FILING DATE: 07/422,801
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 4
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-335-948-4

Query Match      86.6%; Score 759; DB 2; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60

QY 75 FTGLVKYMHSGPVVAMVWEGNLVVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FAGLVKYMHSQPVVAMVWEGNLVVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 135 DSVKSAKEISLWFQPEELVEYKSCAQNWIYE 166
Db 121 DSVESAKEISLWFHPPELVDTYTSCAQNWIYE 152

RESULT 6
US-09-460-532-4
; Sequence 4, Application US/09460532
; Patent No. 6486300
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawking, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,532
; FILING DATE: 13-Dec-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/713,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 468542
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-09-460-532-4

Query Match      86.6%; Score 759; DB 2; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 15 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60

QY 75 FTGLVKYMHSGPVVAMVWEGNLVVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134

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Db 61 FAGLVKYMHSPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
QY 135 DSVKSAEKEISLWFOPEELVEYKSCAQNWIYE 166
Db 121 DSVESAKEIGLWPHFPELVDTYTSQAQNWIYE 152

RESULT 7
US-09-538-092-933
; Sequence 933, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSegFormatter Version 0.9
; SEQ ID NO 933
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P15531
US-09-538-092-933

Query Match 86.6%; Score 759; DB 2; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 15 MANSERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLKKEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLKKEHYTDLKDRPF 60
QY 75 FTGLVKYMHSGPVVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
Db 61 FAGLVKYMHSPPVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
QY 135 DSVKSAEKEISLWFOPEELVEYKSCAQNWIYE 166
Db 121 DSVESAKEIGLWPHFPELVDTYTSQAQNWIYE 152

RESULT 8
US-09-335-948-2
; Sequence 2, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
; APPLICANT: Charles R. King
; APPLICANT: Patricia S. Steeg
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; FILE REFERENCE: 14014.0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/475,634
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR APPLICATION NUMBER: 07/422,801
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-335-948-2
Query Match 83.8%; Score 734; DB 2; Length 176;
Best Local Similarity 90.2%; Pred. No. 2.7e-78;
Matches 138; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 14 TMANSERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLKKEHYTDLKDRP 73
Db 24 TMANLERTFIAIKPDGVQVGLVGEIIRKFEQKGRFLVAMKFLRASSEHLKQHYIDLKDRP 83
QY 74 FTGLVKYMHSGPVVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 133
Db 84 FPGFLVKYMHSGPVVAMVWEGLVNVTGRVLMGETNPADSKPGTIRGDFCIQVGRNIIHGS 143
QY 134 SDSVKSAREKISLWFOPEELVEYKSCAQNWIYE 166
Db 144 SDSVKSAREKISLWFOPEELVEYKSCAQNWIYE 176
RESULT 9
US-07-806-932B-3
; Sequence 3, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:
; APPLICANT: KING, ET AL.
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
; TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI & STEWART
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DM4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/806,932B
; FILING DATE: 11 december 1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,801
; FILING DATE: 18 october 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: CAPELIO, SUSAN A.
; REGISTRATION NUMBER: 34,560
; REFERENCE/DOCKET NUMBER: 469200-72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 AMINO ACID RESIDUES
; TYPE: AMINO ACIDS
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE: HUMAN NM 23-H2S
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM -24 TO 152

US-07-806-932B-3

Query Match 83.8%; Score 734; DB 2; Length 176; *
Best Local Similarity 90.2%; Pred. No. 2.7e-78;
Matches 138; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

[illegible]

RESULT 10

US-08-713-825-5
; Sequence 5, Application US/08713825
; Patent No. 5874285
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/713,825
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0124 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 152 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 127983

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Query Match      83.2%; Score 729; DB 1; Length 152;
Best Local Similarity 90.1%; Pred. No. 8.4e-78;
Matches 137; Conservative 9; Mismatches 6; Indels 0; Gaps 0

QY 15 MANSERTFAIKPDGVQRLGVEIIKTRPEQKGRFLVGLKFLQAGSEDLKHEYTDLKORPF 74
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1  MANLERTFAIKPDGVQRLGVEIIKTRPEQKGRFLVAMKFLRASEEHLKQHYIDLKORPF 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Qy	75	FTGLVKYMHSGPVVAWVWYEGUNVVKTRGVMLGETNPADSKPGTIRGDGFCIQVGRNIHGS	134
Db	61	FPFLVKYMHSGPVVAWVWYEGUNVVKTRGVMLGETNPADSKPGTIRGDGFCIQVGRNIHGS	120
Qy	135	DSVKSAAKEIISLWFOPEELVEYKSCAQNIYYE	166
Db	121	DSVKSAAKEIISLWPKPELVDYKSCAHDWYYE	152

RESULT 11

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US-09-199-842-5
; Sequence 5, Application US/09199842
; Patent No. 6087125
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.5
; CURRENT APPLICATION DATA: US/09/199,842
; APPLICATION NUMBER: US/09/199,842
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,825
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0124 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 127983

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Query Match	83.2%;	Score 729;	DB 2;	Length 152;
Best Local Similarity	90.1%;	Pred. No. 8.4e-78;		
Matches 137;	Conservative	9;	Mismatches 6;	Indels 0; Gaps 0
Qy	15	MANSRTFTAIKPDGVQVGLVEIIKPEQKGFRLVGLKFLQASEDLKELHYTDLKDRPF	74	
Db	1	MANLERTFTAIKPDGVQVGLVEIIKPEQKGFRLVAMKFLRASEEHLKHQYIDLKDRPF	60	
Qy	75	FTGLVKYMHSGPVVAMVWEGNLVNVKTRGVMLGETNPADSKPGTIRGDFCIQVGRNIHGS	134	
Db	61	PFGLVKYMNSGPVVAMVWEGNLVNVKTRGVMLGETNPADSKPGTIRGDFCIQVGRNIHGS	120	
Qy	135	DSVKSAAKEISLWFOPEBLVEYKSCAQNWIIYE	166	
Db	121	DSVKSAAKEISLWFKPEBLVDYKSCAHDWVYE	152	

RESULT 12

Search completed: December 16, 2005, 16:38:12
Job time : 35.4528 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:58 ; Search time 140.528 Seconds
(without alignments)
763.122 Million cell updates/sec

Title: US-10-074-694-5
Perfect score: 803
Sequence: 1 MANLBRTFAIKPDGVRGL.....WFKPELVYKSCAHDWYVE 152

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	803	100.0	152	1 NDKB HUMAN	P22392 homo sapien
2	803	100.0	152	2 Q6FHN3 HUMAN	Q6fhn3 homo sapien
3	795	99.0	152	2 Q5RPH3_PONPY	Q5rph3 pongo pygma
4	794	98.9	152	1 NDKB RAT	P19804 ratus norv
5	793	98.8	152	1 NDKB MOUSE	Q01768 mus musculu
6	793	98.8	152	2 Q5NCB2_MOUSE	Q5ncb2 mus musculu
7	751	93.5	153	2 Q57535_CHICK	Q57535 gallus gall
8	750	93.4	152	2 Q50KA8_CANFA	Q50ka8 canis fami
9	744	92.7	153	1 NDK COLLI	Q90380 columba liv
10	722	91.2	152	1 NDKA RAT	Q05982 ratus norv
11	729	90.8	152	1 NDKA_MOUSE	P15532 mus musculu
12	729	90.8	152	2 Q5NCB1_MOUSE	Q5ncb1 m expressed
13	728	90.7	151	1 NDKB BOVIN	P52175 bos taurus
14	727	90.5	151	1 NDKA BOVIN	P52174 bos taurus
15	725	90.3	152	2 Q56J44_BOVIN	Q56jv4 bos taurus
16	721	89.8	152	1 NDKA CANFA	Q50ka9 canis fami
17	720	89.7	152	1 NDKA HUMAN	P15531 homo sapien
18	720	89.7	152	2 Q6FGK3_HUMAN	Q6fgk3 homo sapien
19	720	89.7	152	2 Q5RC56_PONPY	Q5rc56 pongo pygma
20	720	89.7	176	2 Q80VT7_MOUSE	Q80vt7 mus musculu
21	720	89.7	177	2 Q86XQ2_HUMAN	Q86xq2 homo sapien
22	717	89.3	153	2 Q9DFC0_ICTFU	Q9dfc0 ictalurus p
23	713.5	88.9	153	2 Q99NI2_CAVPO	Q99ni2 cavia porce
24	710	88.4	154	1 NDKA2_XENLA	P70011 xenopus lae
25	710	88.4	154	2 Q5PQ80_XENLA	Q5pq80 xenopus lae
26	706	87.9	153	2 Q7SXG5_BRARE	Q7sxg5 brachydanio
27	705	87.8	153	2 Q9IAD3_BRARE	Q9iad3 brachydanio
28	700	87.2	153	2 Q9PTF5_BRARE	Q9ptf5 brachydanio
29	700	87.2	154	2 P70071_XENLA	P70071 xenopus lae
30	699	87.0	154	2 Q6AZK9_XENTR	Q6azk9 xenopus tro
31	698	86.9	154	1 NDKA1_XENLA	P70010 xenopus lae

32	698	86.9	154	2 Q68FI7_XENLA	Q68fi7 xenopus lae
33	691	86.1	137	1 NDKB HUMAN	O60361 homo sapien
34	666	82.9	151	1 NDK GINCI	P27950 ginglymosto
35	661	82.3	151	2 Q804Y0_ONCMY	Q804y0 oncorhynch
36	656	81.7	151	2 O57560_SALSA	O57560 salmo salar
37	651	81.1	153	2 Q6PC37_BRARE	Q6pc37 brachydanio
38	650	80.9	153	2 Q7SXL4_BRARE	Q7sxl4 brachydanio
39	629.5	78.4	152	2 Q7ZZQ7_OREMO	Q7zzq7 oreochromis
40	620	77.2	152	1 NDKA DROVA	P08879 drosophila
41	616	76.7	150	1 NDKA_MOUSE	Q6xi171 drosophila
42	606	75.5	127	2 Q5NCB0_MOUSE	Q5ncb0 mus musculu
43	596	74.2	153	2 Q7QIX6_ANOGA	Q7qix6 anopheles g
44	594	74.0	365	2 Q8R4B4_MOUSE	Q8r4b4 mus musculu
45	591	73.6	144	2 Q4T9N6_TETNG	Q4t9n6 tetraodon n

ALIGNMENTS

RESULT 1
ID NDKB HUMAN STANDARD; PRT; 152 AA.
AC P22392;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Nucleoside diphosphate kinase B (BC 2.7.4.6) (NDK B) (NDP kinase B)
DE (nm23-H2) (C-myc purine-binding transcription factor PUF).
GN Name=NME2; Synonyms=NM23B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, SUBUNITS, AND ACTIVE SITE.
RX MEDLINE=91224972; PubMed=1851158;
RA Gilles A.-M., Prescan E., Vonica A., Lascau I.;
RT "Nucleoside diphosphate kinase from human erythrocytes. Structural
RT characterization of the two polypeptide chains responsible for
RT heterogeneity of the hexameric enzyme."
RL J. Biol. Chem. 265:8784-8789(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91105674; PubMed=1988104;
RA Stahl J.A., Leone A., Rosengard A.M., Porter L., Liotta L.A.,
RA Steeg P.S., King C.R.;
RT "Identification of a second human nm23 gene, nm23-H2."
RL Cancer Res. 51:445-449(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93324921; PubMed=8392752;
RA Postel E.H., Berberich S.J., Flint S.J., Ferrone C.A.;
RT "Human c-myc transcription factor puf identified as nm23-H2 nucleoside
RT diphosphate kinase, a candidate suppressor of tumor metastasis."
RL Science 261:478-480(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [5]

RL X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RN MEDLINE=95387396; PubMed=7658474;
RP Webb P.A., Perisic O., Mendola C.E., Backer J.M., Williams R.L.; "The crystal structure of a human nucleoside diphosphate kinase, NM23-H2."; J. Mol. Biol. 251:574-587 (1995). [6]

RL X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
RN MEDLINE=96333668; PubMed=8747457; DOI=10.1016/S0969-2126(01)00268-4;
RP Morera S., Lacombe M.-L., Xu Y., Lebras G., Janin J.; "X-ray structure of human nucleoside diphosphate kinase B complexed with GDP at 2-A resolution."; Structure 3:1307-1314 (1995).
RT Structure 3:1307-1314 (1995).
RL -i- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP.
CC -i- FUNCTION: Acts as a transcriptional activator of the c-Myc gene; binds DNA nonspecifically (Ref.3).
CC -i- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.
CC -i- COFACTOR: Magnesium (By similarity).
CC -i- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, ABS, B6).
CC -i- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -i- PTM: The N-terminus is blocked.
CC -i- DISEASE: This protein is found in reduced amount in tumor cells of high metastatic potential.
CC -i- SIMILARITY: Belongs to the NDK family.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; X58965; CAB37870.1; -; mRNA.
DR EMBL; M36981; AAA36369.1; -; mRNA.
CC EMBL; L16785; AAA60228.1; -; mRNA.
DR EMBL; BC002476; AA02476.1; -; mRNA.
DR PIR; A49798; A49798.
DR PDB; 1N5X; X-ray; L/N/O/R/T/U=1-152.
DR PDB; 1NUS; X-ray; A/B/C/D/E/F=2-152.
DR TRANSPAC; T00706; -.
DR OGP; P22392; -.
DR Ensembl; ENSG00000121054; Homo sapiens.
DR HGNC; HGNC:7850; NME2.
DR H-InvDB; HIX0013993; -.
DR Reactome; P22392; -.
DR MIM; 156491; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0005824; P:ATP binding; NAS.
DR GO; GO:0004850; F:nucleoside-diphosphate kinase activity; TAS.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO; GO:0009142; P:nucleoside triphosphate biosynthesis; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF00735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
DR 3D-structure; Activator; Anti-oncogene; ATP-binding; Cell cycle;
KW Direct protein sequencing; DNA-binding; Kinase; Magnesium;

RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN (2)
RP NUCLEOTIDE SEQUENCE.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.,
RT "Cloning of human full-length CDSs in BD Creator (TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN (3)
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Chondrosarcoma;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (4)
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Chondrosarcoma;
RC NIH MGC Project;
RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR541718; CAG46519.1; -; mRNA.
DR EMBL; BT007045; AAP35694.1; -; mRNA.
DR EMBL; BC095458; AAR95458.1; -; mRNA.
DR SMR; O6FHN3; 2-152.
DR Ensembl; ENSG0000121054; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR012005; NDK-2.
DR PIRSF; PIRSF00735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
DR SEQUENCE 152 AA; 17298 MW; 1A5C3F84D7AD272C CRC64;
Query Match 100.0%; Score 803; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 4.6e-70;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANLERTFAIKPDGVQVGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKHQHYIDLKDRPF 60
DB 1 MANLERTFAIKPDGVQVGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKHQHYIDLKDRPF 60
QY 61 FPGVLVKYMSGPPVAMVWVGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FPGVLVKYMSGPPVAMVWVGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 3
QSRFH3_PONPY PRELIMINARY; PRT; 152 AA.
ID QSRFH3_PONPY
AC QSRFH3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp468E0516.
GN Name=DKFZp468E0516;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Han M., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR857184; CAH89484.1; -; mRNA.
DR SMR; QSRFH3; 2-152.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
DR Hypothetical protein.
SQ SEQUENCE 152 AA; 17300 MW; 8D2D9361C94DC938 CRC64;
Query Match 99.0%; Score 795; DB 2; Length 152;
Best Local Similarity 98.7%; Pred. No. 2.8e-69;
Matches 150; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANLERTFAIKPDGVQVGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKHQHYIDLKDRPF 60
DB 1 MANLERTFAIKPDGVQVGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKHQHYIDLKDRPF 60
QY 61 FPGVLVKYMSGPPVAMVWVGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 FPGVLVKYMSGPPVAMVWVGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 4
NDXB_RAT
ID NDXB_RAT
AC P19804;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B)
DE (P18).
GN Name=Nme2;

Rattus norvegicus (Rat).
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
STRAIN=Wistar;
MEDLINE=90368787; PubMed=2168422;
Kimura N., Shimada N., Nomura K., Watanabe K.;
"Isolation and characterization of a cDNA clone encoding rat
nucleoside diphosphate kinase.";
J. Biol. Chem. 265:15744-15749(1990).
[2]
NUCLEOTIDE SEQUENCE.
MEDLINE=92332552; PubMed=13211145;
Ishikawa N., Shinada N., Munakata Y., Watanabe K., Kimura N.;
"Isolation and characterization of a gene encoding rat nucleoside
diphosphate kinase.";
J. Biol. Chem. 267:14366-14372(1992).
[3]
NUCLEOTIDE SEQUENCE.
STRAIN=Sprague-Dawley; TISSUE=Mast cell;
MEDLINE=92256389; PubMed=1316151;
Hemmerich S., Yarden Y., Pecht I.;
"A cromoglycate binding protein from rat mast cells of a leukemia line
is a nucleoside diphosphate kinase.";
Biochemistry 31:4574-4579(1992).
[4]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Brain;
NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
other than ATP. The ATP gamma phosphate is transferred to the NDP
beta phosphate via a ping-pong mechanism, using a phosphorylated
active-site intermediate.
-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
-!- COFACTOR: Magnesium (By similarity).
-!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2,
A3B3, A2B4, AB5, B6).
-!- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Belongs to the NDK family.

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use as long as its content is in no way modified and this statement is not
removed.

EMBL; M55331; AAA41684.1; -; mRNA.
EMBL; M91597; AAA42017.1; -; mRNA.
EMBL; BC086599; AAH86599.1; -; mRNA.
PIR; A41849; A38369.
HSSP; P22392; 1NUE.
SMR; P19804; 2-152.
Ensembl; ENSRNORG0000002671; Rattus norvegicus.
RGD; 619877; Nme2.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDK KINASES; 1.
ATP-binding; Direct protein sequencing; Kinase; Magnesium;
Metal-binding; Nucleotide metabolism; Nucleotide-binding;
Phosphorylation; Transferase.
ACT SITE 118
CONFLICT 89 89 V -> W (in Ref. 3).

SQL	SEQUENCE	152 AA; 17283 MW; 1A5C3F84C1F413EC CRC64;
	Query Match	98.9%; Score 794; DB 1; Length 152;
	Best Local Similarity	98.0%; Pred. No. 3.5e-69;
	Matches 149; Conservative	2; Mismatches 1; Indels 0; Gaps 0
QY	1	MANLERTFTIAIKPDGVORGLVGEIIRKPEQGFRFLVAMKFLRASEEHLKHQHYIDLKDRPF 60
Db	1	MANLERTFTIAIKPDGVORGLVGEIIRKPEQGFRFLVAMKFLRASEEHLKHQHYIDLKDRPF 60
QY	61	FPGLVKYNNGSPVVAMYWEGLNVKTRGVMIGETNPADSKPTGTIRGDFCIOVGRNIHGS 120
Db	61	FPGLVKYNNGSPVVAMYWEGLNVKTRGVMIGETNPADSKPTGTIRGDFCIOVGRNIHGS 120
QY	121	DSVKSABKETSLWFKPEELVDYKSCAHDWVE 152
Db	121	DSVESABKETGLWFKPEELIDYKSCAHDWVE 152
RESULT 5		
ID_NDKB_MOUSE	STANDARD;	PRT; 152 AA.
AC	Q01768;	
DT	01-APR-1993	(Rel. 25, Created)
DT	01-APR-1993	(Rel. 25, Last sequence update)
DE	10-MAY-2005	(Rel. 47, Last annotation update)
DE	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-W2) (PI8).	
DN	Name=Nme2;	
GN	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muridea; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6;	
RC	MEDLINE=92387389; PubMed=1325378; DOI=10.1016/0014-5793(92)80807-S;	
RA	Urano T., Takamiya K., Furukawa K., Shiku H.;	
RT	"Molecular cloning and functional expression of the second mouse	
RT	nm23/NDP kinase gene, nm23-W2."	
RL	FEB8 Lett. 309:358-362 (1992).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6;	
RC	Takeshi U.;	
RA	Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.	
RN	[3]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	
RC	STRAIN=C57BL/6J;	
RC	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;	
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,	
RA	Nikaido I., Osato N., Saico R., Suzuki H., Yamana K.I., Kiyoosawa H.,	
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojbori T.,	
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,	
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,	
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,	
RA	Dalla E.A., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,	
RA	Gaasterland T., Gariboldi M., Gesi C., Godzik A., Gough J.,	
RA	Grimmond S., Gutinchich S., Hirokawa N., Jackson I.J., Jarvis E.D.,	
RA	Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,	
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,	
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,	
RA	Nagasima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,	
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,	
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,	
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,	
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	
RA	Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,	
RA	Wilming L.G., Wyshaw-Boris A., Yangdisawa M., Yang I., Yang L.,	
RA	Xuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,	

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain, and Heart;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
CC other than ATP. The ATP gamma phosphate is transferred to the NDP
CC beta phosphate via a ping-pong mechanism, using a phosphorylated
CC active-site intermediate.
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2,
CC A3B3, A2B4, A5B, B6).
CC -!- SIMILARITY: Belongs to the NDK family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X68193; CAA48275.1; -; mRNA.
DR EMBL; AK012447; BAB28246.1; -; mRNA.
DR EMBL; BC066995; AAH66995.1; -; mRNA.
DR EMBL; BC086892; AAH68892.1; -; mRNA.
DR EMBL; BC086893; AAH68893.1; -; mRNA.
DR PIR; S29241; S29241.
DR HSP; P22392; 1NUE.
DR SMR; Q01768; 2-152.
DR SWISS-2DPAGE; Q01768; MOUSE.
DR PMMA-2DPAGE; Q01768; -.
DR Ensembl; ENSMUSG0000020857; Mus musculus.
DR MGI; MGI:97356; Nme2.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PRINTS; PIRSF000735; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
DR ACT_SITE 118 118 Pros-phosphohistidine intermediate (By

FT SQ SEQUENCE 152 AA; 17363 MW; 1A5C3F84C1FFC83C CRC64; similarity).
Query Match 98.8%; Score 793; DB 1; Length 152;
Best Local Similarity 98.0%; Pred. No. 4.4e-69;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANLERTFTAIKPDGVQVQRLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
|||||
Db 1 MANLERTFTAIKPDGVQVQRLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
QY 61 FPLGLVKYMNKSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
|||||
Db 61 FPLGLVKYMNKSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
|||||
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 6
Q5NC82_MOUSE PRELIMINARY; PRT; 152 AA.
AC Q5NC82;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Expressed in non-metastatic cells 2 protein.
GN ORFNames=RP23-378113.2-002;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mashreghi-Mohammadi M.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL662838; CAI35363.1; -; Genomic_DNA.
DR SMR; Q5NC82; 2-152.
DR Ensembl; ENSMUSG0000020857; Mus musculus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004550; P:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
SQ SEQUENCE 152 AA; 17363 MW; 1A5C3F84C1FFC83C CRC64;
Query Match 98.8%; Score 793; DB 2; Length 152;
Best Local Similarity 98.0%; Pred. No. 4.4e-69;
Matches 149; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANLERTFTAIKPDGVQVQRLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
|||||
Db 1 MANLERTFTAIKPDGVQVQRLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
QY 61 FPLGLVKYMNKSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
|||||
Db 61 FPLGLVKYMNKSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
|||||
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
RESULT 7

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O57535 CHICK
ID O57535 CHICK PRELIMINARY; PRT; 153 AA.
AC O57535;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nucleoside diphosphate kinase.
GN Name=chNDPK;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Mehus J.G., Lambeth D.O.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043542; AAB99856.1; -; mRNA.
DR HSP; P22392; 1NUB.
DR SMR; O57535; 3-153.
DR Ensembl; ENSGALG00000002932; Gallus gallus.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0005524; F:kinase activity; IEA.
DR GO; GO:0016301; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0004550; F:transferase activity; IEA.
DR GO; GO:0016740; F:CTP biosynthesis; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW Kinase.
SQ SEQUENCE 153 AA; 17288 MW; 939DD61D329E008 CRC64;
Query Match 93.5%; Score 751; DB 2; Length 153;
Best Local Similarity 92.7%; Pred. No. 5.4e-65;
Matches 140; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 2 ANLERTFIAIKPDGVQVQGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 61
DB 3 ANCERTFIAIKPDGVQVQGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 62
QY 62 PGLVKTMSGPPVAMWVWGLNVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 121
DB 63 PGLVKTMSGPPVAMWVWGLNVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 122
QY 122 SVKSAEKEISLWFKPEELVDYKSCADHWY 152
DB 123 SVESAQKEISLWFKPAELIDYSCADHWY 153
RESULT 8
Q50KAB CANFA
ID Q50KAB CANFA PRELIMINARY; PRT; 152 AA.
AC Q50KAB;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE NM23-C2.
GN Name=nm23-C2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyoshi N.,
Endo Y., Oishi A., Akuzawa M.;
"Molecular cloning of canine nm23 cDNAs and their expression in normal
and tumor tissues.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB207045; BAD97838.1; -; mRNA.
DR SMR; Q50KAB; 2-152.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
SQ SEQUENCE 152 AA; 17366 MW; 923DA489B37C19C6 CRC64;
Query Match 93.4%; Score 750; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 6.7e-65;
Matches 140; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 MANLERTFIAIKPDGVQVQGLVGEIIRKFEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MAHQERTFIAIKPDGVQVQGLVGEIIRKFEQKGFRLVAMKFLRASEDLKQHYIDLKDRPF 60
QY 61 PGLVKTMSGPPVAMWVWGLNVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120
DB 61 YFGLVKTMSGPPVAMWVWGLNVKTRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 121 DSVKSAEKEISLWFKPEELVDYKSCADHWY 152
DB 121 DSVKSAEKEISLWFKPEELVDYKSCADHWY 152
RESULT 9
NDK COLLI
ID NDK COLLI STANDARD; PRT; 153 AA.
AC Q90380;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase).
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=97450995; PubMed=9305928; DOI=10.1074/jbc.272.39.24604;
Lambeth D.O., Mehus J.G., Ivey M.A., Milavetz B.I.;
"Characterization and cloning of a nucleoside-diphosphate kinase
targeted to matrix of mitochondria in pigeon.";
J. Biol. Chem. 272:24604-24611(1997).
CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
other than ATP. The ATP gamma phosphate is transferred to the NDP
beta phosphate via a ping-pong mechanism, using a phosphorylated
active-site intermediate.
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.
CC -!- TISSUE SPECIFICITY: Highest levels in the liver and kidney with
lower levels in the heart, brain and breast muscle.
CC -!- SIMILARITY: Belongs to the NDK family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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CC EMBL; U61287; AAC60275.1; -; mRNA.
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DR EMBL; AF018266; AAC78437.1; -; Genomic_DNA.
DR HSSP; P22392; INUE.
DR SMR; Q90380; 3-153.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF00735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR PRODOM; PD001018; NDK; 1.
DR PROSITE; PS00469; NDP KINASES; 1.
KW ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism;
KW Nucleotide-binding; Phosphorylation; Transferase.
FT Pro-phosphonistidine intermediate (By similarity).
FT ACT_SITE 119 119
FT SEQUENCE 153 AA; 17299 MW; 4E245D7AE9F0C9EF CRC64;

Query Match          92.7%; Score 744; DB 1; Length 153;
Best Local Similarity 90.7%; Pred. No. 2.6e-64; Indels 0; Gaps 0;
Matches 137; Conservative 9; Mismatches 5;

Qy 2 ANLERTFAIAKPDGVQRGLVGEIIKRFEQKGRFLVAMKFLRASBEHLKHQYVIDLKDRPF 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 ANCERTFAIAKPDGVQRGLVGEIIKRFEQKGRFLVGMKFVHASELLKHQYVIDLKDRPF 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 62 PGLVKYNNSGPVAMVWMEGLNVVKTGRVMLEGTNPADSKPGTTRGDPCIQVGRNIIHGSD 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 PGLVKYNNSGPIVAMVWMEGLNVVKTGRVMLEGTNPADSKPGTTRGDPCIQVGRNIIHGSD 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 122 SVKSAAKEISLMFKPEELVDYKSCAHDWIYE 152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 SVESAQKEINLWFKPASLIIDFKSCAHDWIYE 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
NDKA RAT STANDARD; PRT; 152 AA.
ID CDQ5982;
AC Q05982;
DT 01-FEB-1994 (Rel. 28, Created)
DD DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DE Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
DE DE (tumor metastatic process-associated protein) (Metastasis inhibition factor NM23).
DE GN Name=Nmel;
DN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Rattus.
OX NCBI_TaxID=10116;
OX [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93155067; PubMed=9381409;
RA Shimada N., Ishikawa N., Munakata Y., Toda T., Watanabe K., Kimura N.;
RT "A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolation and characterization of complementary and genomic DNA and expression." J. Biol. Chem. 268:2583-2589(1993).
RL CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.
CC CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.
CC CC -!- COFACTOR: Magnesium (By similarity).
CC CC -!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, AB5, B6). Interacts with SET (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC CC -!- DISEASE: This protein is found in reduced amount in tumor cells of high metastatic potential.
CC CC -!- SIMILARITY: Belongs to the NDK family.
```



```
RP CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC TISSUE=Retina;
RX MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s;
RA Abdulae N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,
RA Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H.,
RA Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;
RT "Nucleoside diphosphate kinase from bovine retina: purification,
RT subcellular localization, molecular cloning, and three-dimensional
RT structure.";
RL Biochemistry 37:13958-13967(1998).
CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
CC other than ATP.
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBUNIT: Homohexamer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and localized to the plasma
CC membrane.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the NDK family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X92957; CAA63533.1; -; mRNA.
DR PDB; 1BE4; X-ray; A/B/C=1-151.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP KINASES; 1.
KW 3D-structure; ATP-binding; Direct protein sequencing; Kinase;
KW Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
KW Nucleotide-binding; Phosphorylation; Transferase.
FT INIT MET 0 0
FT ACT SITE 117 117 Pros-phosphohistidine intermediate.
FT BINDING 11 11 Substrate ATP/NDP ribose.
FT BINDING 59 59 Substrate ATP/NDP base.
FT BINDING 87 87 Substrate ATP/NDP beta phosphate.
FT BINDING 93 93 Substrate ATP/NDP beta phosphate.
FT BINDING 104 104 Substrate ATP/NDP beta phosphate.
FT BINDING 111 111 Substrate ATP/NDP base.
FT BINDING 114 114 Substrate ATP/NDP ribose.
FT BINDING 151 151 Substrate GDP N2.
FT TURN 2 3
FT STRAND 5 10
FT HELIX 12 16
FT TURN 17 18
FT HELIX 20 30
FT TURN 31 31
FT STRAND 33 41
FT HELIX 44 51
FT HELIX 52 54
FT TURN 58 59
FT HELIX 60 62
FT HELIX 63 68
FT STRAND 71 78
FT TURN 80 81
FT HELIX 82 90
FT HELIX 95 97
FT TURN 100 101
FT HELIX 103 107
FT STRAND 110 110
FT TURN 111 112
FT STRAND 113 113
FT TURN 116 118
FT HELIX 122 132

FT HELIX 135 137
FT HELIX 146 149
SQ SEQUENCE 151 AA; 17167 MW; AACDC542C77864E1 CRC64;
Query Match 90.7%; Score 728; DB 1; Length 151;
Best Local Similarity 90.1%; Pred. No. 9.3e-63;
Matches 136; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
QY 2 ANLERTFAIKPDGVORGLVGEIIRKFEQKGRFLVAMKFLRASEHHLAKOHIYIDLKDRPFF 61
DB 1 ANSERTFAIKPDGVORGLVGEIIRKFEQKGRFLVAMKFLRASEHHLAKOHIYIDLKDRPFF 60
QY 62 PGLVKNMNSGVPVAMVWEGNLVVTGTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGSD 121
DB 61 AGLVKYMHSGVPVAMVWEGNLVVTGTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGSD 120
QY 122 SVKSAEKISILWFKPEELVDYKSCAHDWVYE 152
DB 121 SVESAKEITALWFRPEELVNYKSCAQNWYE 151

RESULT 14
NDKA_BOVIN
ID NDKA_BOVIN STANDARD; PRT; 151 AA.
AC P52174;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Nucleoside diphosphate kinase NBR-A (EC 2.7.4.6) (NDK NBR-A) (NDP
DE kinase NBR-A).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT,
RP SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY
RP CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC TISSUE=Retina;
RX MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s;
RA Abdulae N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,
RA Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H.,
RA Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;
RT "Nucleoside diphosphate kinase from bovine retina: purification,
RT subcellular localization, molecular cloning, and three-dimensional
RT structure.";
RL Biochemistry 37:13958-13967(1998).
CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
CC other than ATP.
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBUNIT: Homohexamer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and localized to the plasma
CC membrane.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the NDK family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X92956; CAA63532.1; -; mRNA.
DR PDB; 1BHN; X-ray; A/B/C/D/E/F=1-151.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
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DR SMART; SM00562; NDK; 1.
KW PROSITE; PS00469; NDP_KINASES; 1.
DR 3D-structure; ATP-binding; Direct protein sequencing; Kinase;
KW Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
KW Nucleotide-binding; Phosphorylation; Transferase.
FT INIT_MEI 0
FT ACT_SITE 117 117 ProS-phosphohistidine intermediate.
FT BINDING 11 11 Substrate ATP/NDP ribose.
FT BINDING 59 59 Substrate ATP/NDP base.
FT BINDING 87 87 Substrate ATP/NDP beta phosphate.
FT BINDING 93 93 Substrate ATP/NDP beta phosphate.
FT BINDING 104 104 Substrate ATP/NDP beta phosphate.
FT BINDING 111 111 Substrate ATP/NDP base.
FT BINDING 114 114 Substrate ATP/NDP ribose.
FT BINDING 151 151 Substrate GDP N2.
FT STRAND 5 10
FT HELIX 12 16
FT TURN 17 18
FT HELIX 20 29
FT TURN 30 31
FT STRAND 33 41
FT HELIX 44 50
FT HELIX 52 54
FT TURN 55 56
FT TURN 58 59
FT HELIX 60 69
FT STRAND 71 78
FT TURN 80 81
FT HELIX 82 90
FT TURN 95 97
FT TURN 100 101
FT HELIX 103 107
FT TURN 111 113
FT STRAND 116 118
FT HELIX 122 132
FT TURN 135 137
FT TURN 144 145
FT HELIX 146 149
SQ SEQUENCE 151 AA; 17130 MW; AAD80B21137EA4E1 CRC64;

Query Match 90.5%; Score 727; DB 1; Length 151;
Best Local Similarity 90.1%; Pred. No. 1.2e-62;
Matches 136; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 2 ANLERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 61
DB 1 ANSERFIAIKPDGVQVGLVGEIIRKPEQKGFRLVAMKFWRASEDLLKHEYIDLKDRPF 60

QY 62 PGLVKYMNSGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 121
DB 61 AGLVKYMHSGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120

QY 122 SVKSAEKEISLWFKPEELVDYKSCAHDWYE 152
DB 121 SVESAKEIALWPHPEELVNYKSCAQNWYE 151

RESULT 15
Q56JV4_BOVIN PRELIMINARY; PRT; 152 AA.
AC Q56JV4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE NDP Kinase NBR-A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymphoid;

RA Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;
RT "Analysis of sequences obtained from constructed full-length bovine
CDNA libraries."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY911378; AAW82141.1; -; mRNA.
DR SMR; Q56JV4; 5-152.
DR Ensembl; ENSBTAG0000004651; Bos taurus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006243; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR01564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PRO1243; NUCDPKINASE.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW Kinase.
SQ SEQUENCE 152 AA; 17260 MW; D1DB47DFC731B056 CRC64;

Query Match 90.3%; Score 725; DB 2; Length 152;
Best Local Similarity 89.5%; Pred. No. 1.8e-62;
Matches 136; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MANLERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVAMKFLRASEHLKQHYIDLKDRPF 60
DB 1 MANSERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVAMKFWRASEDLLKHEYIDLKDRPF 60

QY 61 FPGLVKYMNSGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
DB 61 FAGLVKYMHSGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120

QY 121 SVKSAEKEISLWFKPEELVDYKSCAHDWYE 152
DB 121 SVESAKEIALWPHPEELVNYKSCAQNWYE 152

Search completed: December 16, 2005, 16:37:02
Job time : 141.528 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:31:58 ; Search time 153.472 Seconds
(without alignments)
763.122 Million cell updates/sec

Title: US-10-074-694-3

Perfect score: 876

Sequence: 1 QSQPAVKPCHLKGTMANSEK.....WFOPELVEYKSCAQNWIYE 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798	91.1	152	1	NDKA_MOUSE
2	798	91.1	152	1	Q5NC81_MOUSE
3	794	90.6	176	2	Q80VT7_MOUSE
4	779	88.9	152	1	NDKA_RAT
5	774.5	88.4	177	2	Q86XQ2_HUMAN
6	759	86.6	152	1	NDKA_HUMAN
7	759	86.6	152	2	Q6FGK3_HUMAN
8	759	86.6	152	2	Q5RC56_PONPY
9	750	85.6	151	1	NDKA_BOVIN
10	749	85.5	151	1	NKKB_BOVIN
11	748	85.4	152	2	Q56JV4_BOVIN
12	745	85.0	152	1	NDKA_CANFA
13	735	83.9	152	2	Q50KA8_CANFA
14	732.5	83.6	153	2	Q99N12_CAVPO
15	732	83.6	152	2	Q5RFH3_PONPY
16	729	83.2	152	1	NKKB_HUMAN
17	729	83.2	152	2	Q6FHN3_HUMAN
18	720	82.2	152	1	NDKB_RAT
19	719	82.1	152	1	NKKB_MOUSE
20	719	82.1	152	2	Q5NC82_MOUSE
21	714	81.5	153	2	Q9DFC0 ICTPU
22	712	81.3	153	2	Q57535_CHICK
23	710	81.1	153	1	NDK COLLI
24	699	79.8	153	2	Q9IAD3_BRARE
25	699	79.8	153	2	Q7SXG5_BRARE
26	694	79.2	153	2	Q9PTF5_BRARE
27	692	79.0	154	1	NDKA2_XENLA
28	692	79.0	154	2	Q5PQ80_XENLA
29	685	78.2	154	2	P70071_XENLA
30	684	78.1	154	2	Q6AZK9_XENTR
31	683	78.0	154	1	NDKA1_XENLA

32	683	78.0	154	2	Q68FI7_XENLA	Q68fi7 xenopus lae
33	670	76.5	151	2	Q804Y0_ONCMY	Q804y0 oncothymochu
34	666	76.0	151	1	NDK GINGI	P27950 ginglymosto
35	660	75.3	151	2	O57560_SALSA	O57560 salmo salar
36	657	75.0	127	2	O5NC80_MOUSE	O5nc80 mus musculus
37	653	74.5	153	2	Q7SXL4_BRARE	Q7sxl4 brachydanio
38	648	74.0	153	2	Q6PC37_BRARE	Q6pc37 brachydanio
39	628	71.7	137	1	NDK8_HUMAN	O60361 homo sapien
40	628	71.7	152	2	Q7ZZQ7_OREMO	Q7zzq7 oreochromis
41	611	69.7	152	1	NDKA_DROME	P08879 drosophila
42	607	69.3	150	1	NDKA_DROVA	O6xi71 drosophila
43	593	67.7	169	2	Q9PTF3_BRARE	Q9ptf3 brachydanio
44	592	67.6	148	2	Q9PTF4_BRARE	Q9ptf4 brachydanio
45	585	66.8	153	2	Q7QIX6_ANOGA	Q7qix6 anopheles g

ALIGNMENTS

RESULT 1

ID	NDKA_MOUSE	STANDARD;	PRT;	152 AA.
AC	P15532;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DE	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)			
DE	(Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23) (NDPK-A) (nm23-M1).			
GN	Name=Nmel; Synonyms=Nm23;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=90044071; PubMed=2509941; DOI=10.1038/342177a0;			
RA	Rosengard A.M., Krutzsch H.C., Shearn A., Biggs J.R., Barker E.,			
RA	Margulies I.M.K., King C.R., Liotta L.A., Steeg P.S.;			
RT	"Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila development.";			
RL	Nature 342:177-180 (1989).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=88155671; PubMed=3346912;			
RA	Steeg P.S., Bevilacqua G., Kopper L., Thorgeirsson U.P.,			
RA	Talmadge J.E., Liotta L.A., Sobel M.B.;			
RT	"Evidence for a novel gene associated with low tumor metastatic potential.";			
RL	J. Natl. Cancer Inst. 80:200-204 (1988).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=91191558; PubMed=2013093; DOI=10.1016/0092-8674(91)90404-M;			
RA	Leone A., Flatow U., King C.R., Sandeen M.A., Margulies I.M.,			
RA	Liotta L.A., Steeg P.S.;			
RT	"Reduced tumor incidence, metastatic potential, and cytokine responsiveness of nm23-transfected melanoma cells.";			
RL	Cell 65:25-35 (1991).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=129/Sv;			
RA	Dabernat S., Masse K., Daniel J.Y.;			
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Swiss Webster / NIH;			
RA	Gervasi F., Fanciulli M., Lombardi D.;			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	STRAIN=FVB/N; TISSUE=Mammary gland;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Splettenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
CC -1- FUNCTION: Major role in the synthesis of nucleoside triphosphates
CC other than ATP. The ATP gamma phosphate is transferred to the NDP
CC beta phosphate via a ping-pong mechanism, using a phosphorylated
CC active-site intermediate.
CC -1- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2,
CC A3B3, A2B4, A5B, B6). Interacts with SET (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -1- DISEASE: This protein is found in reduced amount in tumor cells of
CC high metastatic potential.
CC -1- SIMILARITY: Belongs to the NDK family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M35970; AAA39826.1; ALT INIT; mRNA.
CC EMBL; M65037; AAA63391.1; -; mRNA.
CC EMBL; U85511; ABA42080.1; -; mRNA.
CC EMBL; AF033377; AAB87689.1; -; mRNA.
CC EMBL; BC005629; AAH05629.1; -; mRNA.
CC PIR; A46557; A46557.
CC HSSP; P15531; 1JXV.
CC SMR; P15532; 5-152.
CC SWISS-2DPAGE; P15532; MOUSE.
CC Ensembl; ENSMUSG00000037601; Mus musculus.
CC MGI; MGI:97355; Nmel.
CC GO; GO:0005792; C:mitosome; IDA.
CC GO; GO:0005625; C:soluble fraction; IDA.
CC InterPro; IPR01564; NDK.
CC InterPro; IPR012005; NDK-2.
CC Pfam; PF00334; NDK; 1.
CC PRSF; PRSF000735; NDK; 1.
CC PRINTS; PD01243; NUCDPKINASE.
CC PRODOM; PD01018; NDK; 1.
CC SMART; SM00562; NDK; 1.
CC PROSITE; PS00469; NDP_KINASES; 1.
KW ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein;
KW Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
KW Transferase.
FT ACT_SITE 118 118 Pro-sphosphohistidine intermediate.
SQ SEQUENCE 152 AA; 17208 MW; EE2E4DB218024686 CRC64;

Query Match 91.1%; Score 798; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.5e-67;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 74
|||||

Db 1 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 60
QY 75 FTGLVKYMSGPPVAMVWGLNVVKTGRVWLGTNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FTGLVKYMSGPPVAMVWGLNVVKTGRVWLGTNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 135 DSVKSAEKISLWFOPEELVEYKSCAQNWIYE 166
Db 121 DSVKSAEKISLWFOPEELVEYKSCAQNWIYE 152

RESULT 2
Q5NC81_MOUSE
ID Q5NC81_MOUSE PRELIMINARY; PRT; 152 AA.
OC Q5NC81_MOUSE
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Expressed in non-metastatic cells 1 protein (12 days embryo embryonic
DE body between diaphragm region and neck cDNA, RIKEN full-length
DE enriched library, clone:9430059B17 product:expressed in non-metastatic
DE cells 1, protein (NM23A) (nucleoside diphosphate kinase), full insert
DE sequence).
GN ORFNames=RP23-378113.1-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mashreghi-Mohammadi M.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gutting S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL662838; CA135364.1; -; Genomic_DNA.
DR EMBL; AK034899; CA28873.1; -; mRNA.
DR SMR; Q5NC81; 5-152.
DR Ensembl; ENSMUSG00000037601; Mus musculus.
GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK-2.
DR InterPro; IPR012005; NDK.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW Kinase.
SQ SEQUENCE 152 AA; 17208 MW; EE2E4DB218024686 CRC64;

Query Match 91.1%; Score 798; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 6.5e-67;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MANSRTFFIAIKPDGVQGLVGEIIKFEQKFLVGLKFLQASEDLKHEHYTLKDRPF 74
Db 1 MANSRTFFIAIKPDGVQGLVGEIIKFEQKFLVGLKFLQASEDLKHEHYTLKDRPF 60

Qy 75 FTGLVKTMHSGPVVAMVWEGVLNVTGRVLMGETNPADSKPTGRTGFCIQVGRNIHGS 134
Db 61 FTGLVKTMHSGPVVAMVWEGVLNVTGRVLMGETNPADSKPTGRTGFCIQVGRNIHGS 120

Qy 135 DSVKSAEKEISLMFQPELVYKSCAQNWIYE 166
Db 121 DSVKSAEKEISLMFQPELVYKSCAQNWIYE 152

RESULT 3
Q80VT7_MOUSE
ID Q80VT7_MOUSE PRELIMINARY; PRT; 176 AA.
AC Q80VT7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nm23 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;

RG NIH MSC Project;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -i- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -i- SIMILARITY: Belongs to the NDK family.
CC EMBL; BC027044; AAH27044.2; -; mRNA.
CC HSSP; P15531; IJUV.
CC SMR; Q80VT7; 28-176.
CC Ensembl; ENSMUSG0000037601; Mus musculus.
CC GO; GO:0005224; F:ATP binding; IEA.
CC GO; GO:0016301; F:kinase activity; IEA.
CC GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006241; P:CTP biosynthesis; IEA.
CC GO; GO:0006183; P:GTP biosynthesis; IEA.
CC GO; GO:0006228; P:UTP biosynthesis; IEA.
CC InterPro; IPR001564; NDK.
CC Pfam; PF00334; NDK; 1.
CC PRINTS; PR01243; NUCDPKINASE.
CC ProDom; PD001018; NDK; 1.
CC SMART; SM00562; NDK; 1.
CC PROSITE; PS00469; NDP_KINASES; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Transferase.
FT NON TER 1
SQ SEQUENCE 176 AA; 19979 MW; 27C36B3DB3F895E3 CRC64;

Query Match 90.6%; Score 794; DB 2; Length 176;
Best Local Similarity 91.5%; Pred. No. 1.8e-66;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 QPAVKCHLKTWANSRTTIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASDILL 62
DB 13 QPEFKPQLSGTWANCERTIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASDILL 72
QY 63 KEHYTLKDRPFFTGLVKYHMSGPVVAMWVGLNVVKTGRVLMGTNPADSKPGTIRGDF 122
DB 73 KEHYVDLKRPFAGLVKYMMSGPVVAMWVGLNVVKTGRVLMGTNPADSKPGTIRGDF 132
QY 123 CIQVGRNIHGSDSVSAEKEISLWFQPEELVYKSCAQNWYE 166
DB 133 CIQVGRNIHGSDSVSAEKEISLWFHPELVDYTSQAQNWYE 176

RESULT 4
NDKA_RAT
ID NDKA_RAT STANDARD; PRT; 152 AA.
AC Q05982;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
DE (tumor metastatic process-associated protein) (Metastasis inhibition factor NM23).
DE Name=Nmel;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93155067; PubMed=8381409;
RA Shimada N., Ishikawa N., Munkata Y., Toda T., Watanabe K., Kimura N.;
RT "A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolation and characterization of complementary and genomic DNA and expression.";
RL J. Biol. Chem. 268:2583-2589 (1993).
CC -i- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.
CC -i- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

CC -i- COFACTOR: Magnesium (By similarity).
CC -i- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B, A2B4, A5, B6). Interacts with SET (By similarity).
CC -i- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -i- DISEASE: This protein is found in reduced amount in tumor cells of high metastatic potential.
CC -i- SIMILARITY: Belongs to the NDK family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; D13374; BAA02635.1; -; mRNA.
CC PIR; A45208; A45208.
CC HSSP; P15531; IJUV.
CC SMR; Q05982; 5-152.
CC Ensembl; ENSRNOG0000002693; Rattus norvegicus.
CC RGD; 70497; Nmel.
CC GO; GO:0005813; C:centrosome; IDA.
CC InterPro; IPR001564; NDK.
CC InterPro; IPR012005; NDK-2.
CC Pfam; PF00334; NDK; 1.
CC PIRSF; PIRSF000735; NDK; 1.
CC PRINTS; PR01243; NUCDPKINASE.
CC ProDom; PD001018; NDK; 1.
CC SMART; SM00562; NDK; 1.
CC PROSITE; PS00469; NDP_KINASES; 1.
KW ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphorylation; Transferase.
FT ACT_SITE 118 118 Pros-phosphohistidine intermediate (By similarity)
SQ SEQUENCE 152 AA; 17193 MW; 32C49E6271195C3B CRC64;

Query Match 88.9%; Score 779; DB 1; Length 152;
Best Local Similarity 96.7%; Pred. No. 4e-65;
Matches 147; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 15 MANSRTTIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLKHEHYTLKDRPF 74
DB 1 MANSRTTIAIKPDGVQVGLVGEIIRKFEQKGRFLVGLKFLQASEDLKHEHYTLKDRPF 60
QY 75 FTGLVKYHMSGPVVAMWVGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134
DB 61 FSGLVKYHMSGPVVAMWVGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120
QY 135 DSVKSAEKEISLWFQPEELVYKSCAQNWYE 166
DB 121 DSVKSAEKEISLWFQPEELVYKSCAQNWYE 152

RESULT 5
Q86XQ2_HUMAN
ID Q86XQ2 HUMAN PRELIMINARY; PRT; 177 AA.
AC Q86XQ2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NM23-H1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22489419; PubMed=12601555; DOI=10.1007/s100380300014;
RA Ni X., Gu S., Dai J., Cheng H., Guo L., Li L., Ji C., Xie Y., Ying K., Mao Y.;
RT "Isolation and characterization of a novel human NM23-H1B gene, a different transcript of NM23-H1.";
RL J. Hum. Genet. 48:96-100 (2003).

[illegible]

RA Fan Z., Beresford P.J., Oh D.Y., Zhang D., Lieberman J.;
 RT "Tumor suppressor NM23-H1 is a granzyme A-activated DNase during CTL-
 RT mediated apoptosis, and the nucleosome assembly protein SET is its
 RT inhibitor."; and the nucleosome assembly protein SET is its
 RN Cell 112:659-672 (2003).
 RN [11]
 RP VARIANT NEUROBLASTOMA GLY-120.
 RX MEDLINE=94322908; PubMed=8047138; DOI=10.1038/370335a0;
 RA Chang C.L., Zhu X.-X., Thoraval D.H., Ungar D., Rawwas J., Hora N.,
 RA Strahler J.R., Hanash S.M.;
 RT "NM23-H1 mutation in neuroblastoma.";
 RL Nature 370:335-336 (1994).
 CC -1- FUNCTION: Major role in the synthesis of nucleoside triphosphates
 CC other than ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
 CC nucleoside triphosphate.
 CC -1- COFACTOR: Magnesium.
 CC -1- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2,
 CC A3B3, A2B4, A5, B6). Interacts with SET.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in lung carcinoma cell lines but not
 CC in normal lung tissues.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: This protein is found in reduced amount in tumor cells of
 CC high metastatic potential. Somatic mutations of NME1 are found in
 CC neuroblastoma. Increased NME1 in neuroblastoma is correlated with
 CC features of the disease that are associated with aggressive
 CC tumors. May therefore have distinct if not opposite roles in
 CC different tumors.
 CC -1- SIMILARITY: Belongs to the NDK family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X17620; CAA35621.1; ALT INIT; mRNA.
 CC EMBL; X75598; CAA53270.1; -; Genomic_DNA.
 CC EMBL; X73066; CAA51527.1; -; mRNA.
 CC EMBL; BC000293; AAH00293.1; -; mRNA.
 CC EMBL; BC018994; AAH18994.1; -; mRNA.
 CC PIR; A33386; A33386.
 CC PDB; 1JXV; X-ray; A/B/C/D/E/F=1-152.
 CC PDB; 1UCN; X-ray; A/B/C=1-152.
 CC Aarhus/Ghent-2DPAGE; 4115; IEF.
 CC Aarhus/Ghent-2DPAGE; 5112; IEF.
 CC OGP; P15531; -.
 CC PMMA-2DPAGE; P15531; -.
 CC Ensembl; ENSG0000011052; Homo sapiens.
 CC HGNC; HGNC:7849; NME1.
 CC H-InvDB; HIX0013992; -.
 CC Reactome; P15531; -.
 CC MIM; 156490; -.
 CC GO; GO:0005634; C:nucleus; NAS.
 CC GO; GO:0005524; F:ATP binding; NAS.
 CC GO; GO:0004536; F:deoxyribonuclease activity; IDA.
 CC GO; GO:0003677; F:DNA binding; IC.
 CC GO; GO:0000287; F:magnesium ion binding; IDA.
 CC GO; GO:0004550; F:nucleoside-diphosphate kinase activity; NAS.
 CC GO; GO:0008285; F:negative regulation of cell proliferation; TAS.
 CC GO; GO:0009142; P:nucleoside triphosphate biosynthesis; NAS.
 CC InterPro; IPR001564; NDK.
 CC InterPro; IPR012005; NDK-2.
 CC Pfam; PF00334; NDK; 1.
 CC PRSF; PRSF000735; NDK; 1.
 CC PRINTS; PR01243; NUCDPKINASE.
 CC ProDom; PD001018; NDK; 1.
 CC SMART; SM00562; NDK; 1.
 CC PROSITE; PS00469; NDP_KINASES; 1.
 KW 3D-structure; Anti-oncogene; ATP-binding; Cell cycle;
 KW Direct protein sequencing; Disease mutation; Kinase; Magnesium;
 KW Metal-binding; Nuclear protein; Nucleotide metabolism;

KW Nucleotide-binding; Phosphorylation; Transferase.
 RT ACT SITE 118 118 Pros-phosphohistidine intermediate.
 FT BINDING 12 12 Substrate ATP/NDP ribose.
 FT BINDING 60 60 Substrate ATP/NDP base.
 FT BINDING 88 88 Substrate ATP/NDP beta phosphate.
 FT BINDING 94 94 Substrate ATP/NDP beta phosphate.
 FT BINDING 105 105 Substrate ATP/NDP base.
 FT BINDING 112 112 Substrate ATP/NDP base.
 FT BINDING 115 115 Substrate ATP/NDP ribose.
 FT BINDING 152 152 Substrate GDP N2.
 FT VARIANT 120 120 S -> G (in neuroblastoma).
 FT /FTIDVAR 004625.
 FT F->W: No loss of activity or substrate
 FT binding.
 FT H->G: Loss of activity.
 FT MUTAGEN 60 60
 FT MUTAGEN 118 118
 FT STRAND 6 11
 FT HELIX 13 17
 FT TURN 18 19
 FT HELIX 21 31
 FT TURN 32 32
 FT STRAND 34 41
 Query Match 86.6%; Score 759; DB 1; Length 152;
 Best Local Similarity 94.1%; Pred. No. 3e-63;
 Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 15 MANSERTFAIKPDGVQGVGLVGEIIKRFQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 74
 DB 1 MANSERTFAIKPDGVQGVGLVGEIIKRFQKGFRLVGLKFLQASEDLKKEHYTDLKDRPF 60
 QY 75 FTGLVYMHSGPVVAMVMEGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 134
 DB 61 FAGLVYMHSGPVVAMVMEGLNVVKTGRVLMGTNPADSKPGTIRGDFCIQVGRNIHGS 120
 QY 135 DSVKSAKEISLMFQPEELVEYKSCAQNWIYE 166
 DB 121 DSVESAKEISLMFQPEELVEYKSCAQNWIYE 152
 RESULT 7
 Q6FGK3 HUMAN
 ID Q6FGK3_HUMAN PRELIMINARY; PRT; 152 AA.
 AC Q6FGK3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE NME1 protein.
 GN Name=NME1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., LaBaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR542104; CAG46901.1; -; mRNA.
 DR EMBL; CR542115; CAG46912.1; -; mRNA.
 DR SMR; Q6FGK3; 4-152.
 DR Ensembl; ENSG00000011052; Homo sapiens.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006241; P:CTP biosynthesis; IEA.
 DR GO; GO:0006183; P:GTP biosynthesis; IEA.
 DR GO; GO:0006228; P:UTP biosynthesis; IEA.
 DR InterPro; IPR001564; NDK.
 DR InterPro; IPR012005; NDK-2.
 DR Pfam; PF00334; NDK; 1.

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DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR SMART; SMO0562; NDK; 1.
DR PROSITE; PS00469; NDP KINASES; 1.
SQ SEQUENCE 152 AA; 17149 MW; AAE9CODF63CB70A1 CRC64;

Query Match
Best Local Similarity 94.1%; Score 759; DB 2; Length 152;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 15 MANSERTFIATKPGVORGLVGEIIRKPEQKGRVLGKFLQASEDLKKEHYTLKDRPF 74
Db 1 MANSERTFIATKPGVORGLVGEIIRKPEQKGRVLGKFLQASEDLKKEHYTLKDRPF 60
Qy 75 FTGLVKYMHSGPVVAMVWEGVLNVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FAGLVKYMHSQPVVAMVWEGVLNVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 135 DSVKSAEKEISLWFOPELVEYKSCAQNWIVE 166
Db 121 DSVESAEEKIGLWHPPELVDTYTSQAQNWIVE 152

RESULT 8
Q5RC56 PONPY PRELIMINARY; PRT; 152 AA.
AC Q5RC56;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DRFZp46800911.
GN Name=DKFZp46800911;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
NCBI_TaxID=9600;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858425; CAH90654.1; -; mRNA.
DR SMR; Q5RC56; 4-152
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR01564; NDK.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SMO0562; NDK; 1.
DR PROSITE; PS00469; NDP KINASES; 1.
KW Hypothetical protein.
SQ SEQUENCE 152 AA; 17149 MW; AAE9CODF63CB70A1 CRC64;

Query Match
Best Local Similarity 94.1%; Score 759; DB 2; Length 152;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 15 MANSERTFIATKPGVORGLVGEIIRKPEQKGRVLGKFLQASEDLKKEHYTLKDRPF 74
Db 1 MANSERTFIATKPGVORGLVGEIIRKPEQKGRVLGKFLQASEDLKKEHYTLKDRPF 60
Qy 75 FTGLVKYMHSGPVVAMVWEGVLNVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
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Db 61 FAGLVKYMHSQPVVAMVWEGVLNVKTRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120
Qy 135 DSVKSAEKEISLWFOPELVEYKSCAQNWIVE 166
Db 121 DSVESAEEKIGLWHPPELVDTYTSQAQNWIVE 152

RESULT 9
NDKA BOVIN STANDARD; PRT; 151 AA.
AC P52174;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Nucleoside diphosphate kinase NBR-A (EC 2.7.4.6) (NDK NBR-A) (NDP kinase NBR-A).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
RN PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT,
RP SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY
RC CRYSTALLOGRAPHY (2.4 ANGSTROMS).
TX TISSUE=Retina;
MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s;
Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,
Yakhyayev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H.,
Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;
"Nucleoside diphosphate kinase from bovine retina: purification,
subcellular localization, molecular cloning, and three-dimensional
structure.";
RT Biochemistry 37:13958-13967(1998).
RL Biochemistry 37:13958-13967(1998).
CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
other than ATP.
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBUNIT: Homohexamer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and localized to the plasma
membrane.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the NDK family.
-----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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EMBL; X92956; CAA63532.1; -; mRNA.
PDB; 1BHN; X-ray; A/B/C/D/E/F=1-151.
InterPro; IPR01564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SMO0562; NDK; 1.
PROSITE; PS00469; NDP KINASES; 1.
3D-structure; ATP-binding; Direct protein sequencing; Kinase;
Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
Nucleotide-binding; Phosphorylation; Transferase.
KW INIT_MET 0
FT ACT_SITE 117 117 Pros-phosphohistidine intermediate.
FT BINDING 11 11 Substrate ATP/NDP ribose.
FT BINDING 59 59 Substrate ATP/NDP base.
FT BINDING 87 87 Substrate ATP/NDP beta phosphate.
FT BINDING 93 93 Substrate ATP/NDP beta phosphate.
FT BINDING 104 104 Substrate ATP/NDP beta phosphate.
FT BINDING 111 111 Substrate ATP/NDP base.
```

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FT BINDING 114 Substrate ATP/NDP ribose.
FT BINDING 151 Substrate GDP N2.
FT STRAND 5 10
FT HELIX 12 16
FT TURN 17 18
FT TURN 20 29
FT TURN 30 31
FT STRAND 33 41
FT HELIX 44 50
FT HELIX 52 54
FT TURN 55 56
FT TURN 58 59
FT HELIX 60 69
FT STRAND 71 78
FT TURN 80 81
FT HELIX 82 90
FT TURN 95 97
FT TURN 100 101
FT HELIX 103 107
FT TURN 111 113
FT STRAND 116 118
FT HELIX 122 132
FT HELIX 135 137
FT TURN 144 145
FT HELIX 146 149
SQ SEQUENCE 151 AA; 17130 MW; AAD80B21137EA4E1 CRC64;

Query Match 85.6%; Score 750; DB 1; Length 151;
Best Local Similarity 92.7%; Pred. No. 2.1e-62;
Matches 140; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 16 ANSERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPFF 75
Db 1 ANSERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPFF 60

Qy 76 TGLVKYMHSGPVVAMVWVGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 135
Db 61 AGLVKYMHSGPVVAMVWVGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

Qy 136 SVKSAEKISLWQPELVKYKCAQNWIYE 166
Db 121 SVESAEEKIALWFHPELVNYKCAQNWIYE 151

RESULT 10
NDKB_BOVIN STANDARD; PRT; 151 AA.
AC P52175;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Nucleoside diphosphate kinase NBR-B (EC 2.7.4.6) (NDK NBR-B) (NDP
DE kinase NBR-B).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT,
RP SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY
RP CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC TISSUE=Retina;
RX MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s;
RA Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,
RA Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H.,
RA Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;
RT "Nucleoside diphosphate kinase from bovine retina: purification,
RT subcellular localization, molecular cloning, and three-dimensional
RT structure.";
RL Biochemistry 37:13958-13967(1998).
CC -1- FUNCTION: Major role in the synthesis of nucleoside triphosphates
other than ATP.
```

```
CC -1- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -1- COPACTOR: Magnesium (By similarity).
CC -1- SUBUNIT: Homohexamer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and localized to the plasma
CC membrane.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the NDK family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X92957; CAA63533.1; -; mRNA.
CC PDB; 1BE4; X-ray; A/B/C=1-151.
CC InterPro; IPR001564; NDK.
CC InterPro; IPR012005; NDK-2.
CC Pfam; PF00334; NDK; 1.
CC PIRSF; PIRSF000735; NDK; 1.
CC PRINTS; PR01243; NUCDEKINASE.
CC ProDom; PD001018; NDK; 1.
CC SMART; SM00562; NDK; 1.
CC PROSITE; PS00469; NDP_KINASES; 1.
CC 3D-structure; ATP-binding; Direct protein sequencing; Kinase;
CC Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
CC Nucleotide-binding; Phosphorylation; Transferase.
CC INIT MET 0 0
CC FT ACT SITE 117 117 Pros-phosphohistidine intermediate.
CC FT BINDING 11 11 Substrate ATP/NDP ribose.
CC FT BINDING 59 59 Substrate ATP/NDP base.
CC FT BINDING 87 87 Substrate ATP/NDP beta phosphate.
CC FT BINDING 93 93 Substrate ATP/NDP beta phosphate.
CC FT BINDING 104 104 Substrate ATP/NDP beta phosphate.
CC FT BINDING 111 111 Substrate ATP/NDP base.
CC FT BINDING 114 114 Substrate ATP/NDP ribose.
CC FT BINDING 151 151 Substrate GDP N2.
CC FT STRAND 2 3
CC FT HELIX 5 10
CC FT TURN 12 16
CC FT TURN 17 18
CC FT HELIX 20 30
CC FT TURN 31 31
CC FT STRAND 33 41
CC FT HELIX 44 51
CC FT HELIX 52 54
CC FT TURN 58 59
CC FT HELIX 60 62
CC FT HELIX 63 68
CC FT STRAND 71 78
CC FT TURN 80 81
CC FT HELIX 82 90
CC FT HELIX 95 97
CC FT TURN 100 101
CC FT HELIX 103 107
CC FT STRAND 110 110
CC FT TURN 111 112
CC FT STRAND 113 113
CC FT STRAND 116 118
CC FT HELIX 122 132
CC FT HELIX 135 137
CC FT HELIX 146 149
CC SQ SEQUENCE 151 AA; 17167 MW; AACDC542C77864E1 CRC64;

Query Match 85.5%; Score 749; DB 1; Length 151;
Best Local Similarity 92.7%; Pred. No. 2.6e-62;
Matches 140; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 16 ANSERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPFF 75
Db 1 ANSERTFIAIKPDGVQVGLVGEIIRKPEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPFF 60
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QY 76 TGLVKYHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 135
Db 61 AGLVKYHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 136 SVKSAEKEISLWFQPEELVYKSCAQNWIYE 166
Db 121 SVESAKEKEIALWFPPEELVYKSCAQNWIYE 151

RESULT 11
Q56JV4_BOVIN
ID Q56JV4_BOVIN PRELIMINARY; PRT; 152 AA.
AC Q56JV4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE NUP kinase NBR-A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymphoid;
RA Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;
RT "Analysis of sequences obtained from constructed full-length bovine
  cDNA libraries".
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY911378; AAW82141.1; -; mRNA.
DR SMR; Q56JV4; 5-152.
DR Ensembl; ENSBTAG0000004651; Bos taurus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW Kinase.
SQ SEQUENCE 152 AA; 17260 MW; D1DB47DFC731B056 CRC64;

Query Match 85.4%; Score 748; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 3.3e-62;
Matches 140; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKWRASEDLKHEHYIDLKDRPF 60

QY 75 FTGLVKYHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FAGLVKYMHSQSPVAVMWVEGLNVVKTGRVLMGETNPADSKPGTIHGDGFCIQVGRNIHGS 120

QY 135 DSVKSAEKEISLWFQPEELVYKSCAQNWIYE 166
Db 121 DSVESAKEKEIALWFPPEELVYKSCAQNWIYE 152

RESULT 12
NDKA_CANFA
ID NDKA_CANFA STANDARD; PRT; 152 AA.
AC Q50KA9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE NM23-C2.
GN Name=nm23-C2;
```

```
DE Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
  (nm23-C1).
DE Name=NMEL;
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Takahashi M., Ume R., Fukushima K., Fujiki M., Misumi K., Miyoshi N.,
  Endo Y., Oishi A., Akuzawa M.;
RT "Molecular cloning of canine nm23 cDNAs and their expression in normal
  and tumor tissues.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
  other than ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
  nucleoside triphosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBUNIT: Hexamer of two different chains: A and B (A6, ASB, A4B2,
  A3B3, A2B4, AB5, B6). Interacts with SET (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the NDK family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.
CC -----
CC EMBL; AB207044; BAD97837.1; -; mRNA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR PRODOM; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein;
  Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
  Transferase.
KW FT
KW ACT_SITE 118 118 Pros-phosphohistidine intermediate (By
  similarity).
SQ SEQUENCE 152 AA; 17180 MW; 669D444D69380FE6 CRC64;

Query Match 85.0%; Score 745; DB 1; Length 152;
Best Local Similarity 92.1%; Pred. No. 6.3e-62;
Matches 140; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MANSERTFIAIKPDGVQGLVGEIIRKFEQKGFRLVAMKLIQASEDLKHEHYIDLKDRPF 60

QY 75 FTGLVKYHSGPVVAMWVEGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FAGLVKYMHSQSPVAVMWVEGLNVVKTGRVLMGETNPADSKPGTIHGDGFCIQVGRNIHGS 120

QY 135 DSVKSAEKEISLWFQPEELVYKSCAQNWIYE 166
Db 121 DSVESAKEKEIQLWFPPEELVYKSCAQNWIYE 152

RESULT 13
Q50KA8_CANFA
ID Q50KA8_CANFA PRELIMINARY; PRT; 152 AA.
AC Q50KA8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE NM23-C2.
GN Name=nm23-C2;
```

```
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyoshi N.,
RA Endo Y., Oishi A., Akuzawa M.;
RT "Molecular cloning of canine nm23 cDNAs and their expression in normal
RT and tumor tissues.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB207045; BAD97838.1; -; mRNA.
DR SMR; Q50KAB; 2-152.
DR InterPro; IPR012005; NDK-2.
DR PIRSF; PF00334; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
SQ SEQUENCE 152 AA; 17366 MW; 923DA489B37C19C6 CRC64;

Query Match 83.9%; Score 735; DB 2; Length 152;
Best Local Similarity 90.1%; Pred. No. 5.5e-61;
Matches 137; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 15 MANSERTFIAIKPDGVQVGLVGVIIKRFQKGLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MAHQRTFIAIKPDGVQVGLVGVIIKRFQKGLVGLKFLQASEDLKHEHYTDLKDRPF 60

QY 75 FTGLVKYMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 YPGLVKYMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 135 DSVKSAEKEISLWFOPEELVEYKSCAQNWIYE 166
Db 121 DSVKSAEKEISLWFKPEELVDYKSCAFDWIYE 152

RESULT 14
Q99NI2_CAVPO
ID Q99NI2_CAVPO PRELIMINARY; PRT; 153 AA.
AC Q99NI2_CAVPO (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Nucleoside diphosphate kinase A.
GN Name=NDPK-A;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cardiac endothelium;
RA Buxton I.L.O.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cardiac endothelium;
RA Buxton I.L.O., Kaiser R.A., Oxhorn B.C., Cheek D.J.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the NDK family.
DR EMBL; AY017306; AAK00527.1; -; mRNA.
DR HSP; P15531; LUXV.
DR SMR; Q99NI2; 5-153.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
```

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DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR KINASE.
SQ SEQUENCE 153 AA; 17198 MW; 9E1FB7F2C4C1C844 CRC64;

Query Match 83.6%; Score 732.5; DB 2; Length 153;
Best Local Similarity 90.8%; Pred. No. 9.5e-61;
Matches 139; Conservative 9; Mismatches 4; Indels 1; Gaps 1;

QY 15 MANSERTFIAIKPDGVQVGLVGVIIKRFQKGLVGLKFLQASEDLKHEHYTDLKDRPF 74
Db 1 MASSERTFIAIKPDGVQVGLVGVIIKRFQKGLVGLKFLQASEDLKHEHYTDLKDRPF 60

QY 75 FTGLVKYMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 134
Db 61 FPLGLVKYMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS 120

QY 135 -DSVKSAREISLWFOPEELVEYKSCAQNWIYE 166
Db 121 GDSVESAREIALWFOPEELVDYRSCAQDWIYE 153

RESULT 15
Q5RPH3_PONPY
ID Q5RPH3_PONPY PRELIMINARY; PRT; 152 AA.
AC Q5RPH3_PONPY (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp468E0516.
GN Name=DKFZp468E0516;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857184; CAH89484.1; -; mRNA.
DR SMR; Q5RPH3; 2-152.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006241; P:CTP biosynthesis; IEA.
DR GO; GO:0006183; P:GTP biosynthesis; IEA.
DR GO; GO:0006228; P:UTP biosynthesis; IEA.
DR InterPro; IPR001564; NDK.
DR InterPro; IPR012005; NDK-2.
DR Pfam; PF00334; NDK; 1.
DR PIRSF; PIRSF000735; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
DR Hypothetical protein_
SQ SEQUENCE 152 AA; 17300 MW; 8D2D9361C94DC938 CRC64;

Query Match 83.6%; Score 732; DB 2; Length 152;
Best Local Similarity 90.1%; Pred. No. 1e-60;
Matches 137; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
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Qy	15	MANSERTFIAIKPDGVQVORGLVGEIIRKFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF	74
Db	1	MANLERTFIAIKPDGVQVORGLVGEIIRKFEQKGFRLVAMKFLRASEEHLKQHYTDLKDRPF	60
Qy	75	FTGLVKYMHSGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS	134
Db	61	FPGLVKYMNSGPVVAMVWEGLVNVTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS	120
Qy	135	DSVKSAREKISLWFQPEELVEYKSCAONWIYE	166
Db	121	DSVKSAREKISLWFQPEELVDYKSCAHDWYE	152

Search completed: December 16, 2005, 16:37:01
Job time : 155.472 secs

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Result No.	Score	Query		DB	ID	Description
		Match	%			
1	794	90.6	184	2	US-09-335-948-5	Sequence 5, Appli
2	794	90.6	184	2	US-07-806-932B-1	Sequence 1, Appli
3	759	86.6	152	1	US-08-713-825-4	Sequence 4, Appli
4	759	86.6	152	2	US-09-199-842-4	Sequence 4, Appli
5	759	86.6	152	2	US-09-335-948-4	Sequence 4, Appli
6	759	86.6	152	2	US-09-460-532-4	Sequence 4, Appli
7	759	86.6	152	2	US-09-538-092-933	Sequence 933, App
8	734	83.8	176	2	US-09-335-948-2	Sequence 2, Appli
9	734	83.8	176	2	US-07-806-932B-3	Sequence 3, Appli
10	729	83.2	152	1	US-08-713-825-5	Sequence 5, Appli
11	729	83.2	152	2	US-09-199-842-5	Sequence 5, Appli
12	729	83.2	152	2	US-09-335-948-1	Sequence 1, Appli
13	729	83.2	152	2	US-09-460-532-5	Sequence 5, Appli
14	729	83.2	152	2	US-09-538-092-987	Sequence 987, App
15	547.5	62.5	168	1	US-08-667-023-2	Sequence 2, Appli
16	547.5	62.5	168	1	US-08-713-825-3	Sequence 3, Appli
17	547.5	62.5	168	2	US-09-199-842-3	Sequence 3, Appli
18	547.5	62.5	168	2	US-09-460-532-3	Sequence 3, Appli
19	542	61.9	117	2	US-09-513-999C-5323	Sequence 5323, Ap
20	531	60.6	153	2	US-09-348-796A-18029	Sequence 18029, A
21	526	60.0	151	2	US-09-183-861-20	Sequence 20, Appl
22	526	60.0	151	2	US-09-022-765-20	Sequence 20, Appl
23	526	60.0	151	2	US-09-551-974B-20	Sequence 20, Appl
24	526	60.0	151	2	US-09-365-501A-20	Sequence 20, Appl
25	526	60.0	151	2	US-09-639-206A-20	Sequence 20, Appl
26	526	60.0	151	2	US-09-874-923-20	Sequence 20, Appl
27	526	60.0	151	2	US-08-798-841-20	Sequence 20, Appl

APPLICANT: KING, ET AL.
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI & STEWART
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989

ATTORNEY/AGENT INFORMATION:

NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 184 AMINO ACID RESIDUES
TYPE: AMINO ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE: HUMAN NM 23-H28

PUBLICATION INFORMATION:

US-07-806-932B-1
PUBLICATION INFORMATION: 1: FROM -32 TO 152

Query Match 90.6%; Score 794; DB 2; Length 184;
Best Local Similarity 91.5%; Pred. No. 2.4e-85;
Matches 150; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY	3	QPAVKPCHLKGTMANSERTFIAIKPDGVQRLVGLVGLKFLQASDILL	62
DB	21	QPOFKPKQLEGTMANCERTFIAIKPDGVQRLVGLVGLKFLQASDILL	80
QY	63	KEHYTDLKORPFTGLVKVMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDF	122
DB	81	KEHYDVKORPFFAGLVKVMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDF	140
QY	123	CIQVGRNIHSGSVSAEKEISLWFQPEELVEVKSQAQNIWE	166
DB	141	CIQVGRNIHSGSVSAEKEISLWFHPEELVDYTSQAQNIWE	184

RESULT 3

US-08-713-825-4
Sequence 4, Application US/08713825
Patent No. 5874285
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/713,825

FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0124 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 152 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 468542

US-08-713-825-4

Query Match 86.6%; Score 759; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY	15	MANSERTFIAIKPDGVQRLVGLVGLKFLQASDILLKEHYTDLKDRPF	74
DB	1	MANCERTFIAIKPDGVQRLVGLVGLKFLQASDILLKEHYTDLKDRPF	60
QY	75	FTGLVKVMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS	134
DB	61	FAGLVKVMHSGPVVAMVWGLNVVKTGRVLMGETNPADSKPGTIRGDFCIQVGRNIHGS	120
QY	135	DSVKSAREKISLWFQPEELVEVKSQAQNIWE	166
DB	121	DSVESAREKISLWFHPEELVDYTSQAQNIWE	152

RESULT 4

US-09-199-842-4
Sequence 4, Application US/09199842
Patent No. 6087125

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

